

From: Mertz, Prema
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Prema Mertz, Ph.D.
Primary Examiner
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Patent Family: _____
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Questel/Orbit: _____
DRLink: _____
Lexis/Nexis: _____
Sequence Sys.: _____
WWW/Internet: _____
Other (specify): _____

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Result No.	Score	Query Match	Length	DB ID	Description
1	2275	100.0	422	4 Q16542	Q16542 homo sapien
2	1897	83.4	432	11 Q64385	Q64385 mus musculu
3	1871	82.2	432	11 P70225	P70225 mus musculu
4	1860.5	81.8	431	11 Q99mf4	Q99mf4 ratus norv
5	391	17.2	372	11 Q88507	Q88507 mus musculu
6	269	11.8	228	11 Q35228	Q35228 mus musculu
7	259.5	11.4	229	4 Q7269	Q7269 homo sapien
8	255.5	11.2	229	4 Q14213	Q14213 homo sapien
9	215.5	9.5	881	13 Q57519	Q57519 xenopus lae
10	211.5	9.3	422	4 Q75462	Q75462 homo sapien
11	210.5	9.3	422	4 Q9UH5	Q9UH5 homo sapien
12	209.5	9.2	425	11 Q9jm58	Q9jm58 mus musculu
13	192	8.4	227	6 Q9GIW3	Q9GIW3 ursus marit
14	191	8.4	327	11 Q9et05	Q9et05 martota mon
15	190.5	8.4	206	4 Q16354	Q16354 homo sapien
16	190.5	8.4	268	4 Q8Tcd78	Q8Tcd78 homo sapien

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2275	100.0	422	4 Q16542	Q16542 homo sapien
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9	215.5	9.5	881	13 Q57519	Q57519 xenopus lae
10	211.5	9.3	422	4 Q75462	Q75462 homo sapien
11	210.5	9.3	422	4 Q9UH5	Q9UH5 homo sapien
12	209.5	9.2	425	11 Q9jm58	Q9jm58 mus musculu
13	192	8.4	227	6 Q9GIW3	Q9GIW3 ursus marit
14	191	8.4	327	11 Q9et05	Q9et05 martota mon
15	190.5	8.4	206	4 Q16354	Q16354 homo sapien
16	190.5	8.4	268	4 Q8Tcd78	Q8Tcd78 homo sapien

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9	215.5	9.5	881	13 Q57519	Q57519 xenopus lae
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11	210.5	9.3	422	4 Q9UH5	Q9UH5 homo sapien
12	209.5	9.2	425	11 Q9jm58	Q9jm58 mus musculu
13	192	8.4	227	6 Q9GIW3	Q9GIW3 ursus marit
14	191	8.4	327	11 Q9et05	Q9et05 martota mon
15	190.5	8.4	206	4 Q16354	Q16354 homo sapien
16	190.5	8.4	268	4 Q8Tcd78	Q8Tcd78 homo sapien

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3	1871	82.2	432	11 P70225	P70225 mus musculu
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12	209.5	9.2	425	11 Q9jm58	Q9jm58 mus musculu
13	192	8.4	227	6 Q9GIW3	Q9GIW3 ursus marit
14	191	8.4	327	11 Q9et05	Q9et05 martota mon
15	190.5	8.4	206	4 Q16354	Q16354 homo sapien
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Result No.	Score	Query Match	Length	DB ID	Description
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13	192	8.4	227	6 Q9GIW3	Q9GIW3 ursus marit
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15	190.5	8.4	206	4 Q16354	Q16354 homo sapien
16	190.5	8.4	268	4 Q8Tcd78	Q8Tcd78 homo sapien

OX	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
RN	[1] NCBI_TAXID=10116;	
RC	SEQUENCE FROM N.A.	
RA	"Expression of interleukin-11 and interleukin-11 receptor alpha chain in the rat uterus in the peri-implantation period.";	
RT	Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.	
DR	EMBL: AF347936; AAK29624; 1; -.	
DR	HSSP; P16471; 1BP3.	
DR	InterPro; IPR002996; CRIA.	
DR	InterPro; IPR003961; FN_III.	
DR	InterPro; IPR003550; Hemtopoptn_L_F3.	
DR	InterPro; IPR003590; Ig.	
DR	InterPro; IPR003600; Ig_like.	
DR	InterPro; IPR003006; Ig_MHC.	
DR	Pfam; PF00041; fn3; 2.	
DR	PFan; PF00047; ig; 1.	
DR	SMART; SM00050; FN3; 2.	
DR	SMART; SM00409; Ig; 1.	
DR	SMART; SM00410; Ig_like; 1.	
DR	PROSITE; PS01354; HEMATopo_REC_L_F3; UNKNOWN_1.	
KW	DR	PROSITE; PS01354; HEMATopo_REC_L_F3; UNKNOWN_1.
RECEPTOR	DR	PROSITE; PS01354; HEMATopo_REC_L_F3; UNKNOWN_1.
SQ	431 AA; 45784 MW; E086FD6B1688180B CRC64;	
Query Match	81.8%; Score 1860.5; DB 11; Length 431;	
Best Local Similarity	82.0%; Pred. No. 6.3e-135;	
Matches	347; Conservative 21; Mismatches 54; Indels 1; Gaps 1;	
Qy	1 MSSSSGLSRVLYAVATALVASSSPCCPOAWGPGVQYQGPGRSVKLCCPGVYTAGDPVSWF 60	
Db	1 MSSSSRLGTRVLYAVATALVSSSTPCQAWGPGVQYQGPGRSVKLCCPGVYTAGDPVSWF 60	
Qy	61 RQDGPKLQGPDSLGHFLVLQAQDSDEGTYCOTDGALGTVTLQLGYPPARPVSC 120	
Db	61 RQDGSRLLQGPDSLGHFLVLQAQDSRDEGTYCRTLGDVGFMVTLKLGSMPAREVSC 120	
Qy	121 QADDYENFSCTWSPSQTSIGLPRLYLTSYRKTKYLQADSDQRSPSTGPWPCCPDPLGARC 180	
Db	121 QADYENFSCTWSPSQTSIGLPRLYLTSYRKTKYLQADSDQRSPSTGPWPCCPDPLGARC 180	
Qy	181 VHGAEFMSQYRINTEVNPLGASTRLDVQSQSLIRPDPGQLRVEVSVPGVYPRRLASW 240	
Db	181 VHGAEFMSQYRINTEVNPLGASTCLDVRQRLRDPDPGQLRVEVSVPGVYPRRLASW 240	
Qy	241 TPAWSWQPHFLKFLKFLQYRAQHPWSTVPAQLEEVITDAVGLPHAVRSARDFLD 300	
Db	241 TPAWSWQPHFLKFLKFLQYRAQHPWSTVPAQLEEVITDAVGLPHAVRSARDFLD 300	
Qy	301 AGTWSTSPEANQTPSTGTIPKEIPAMQQLHTQP-EVEPOVQSPAPRPSLQPHPRLDH 359	
Db	301 AGTWSANSPEANQTPSTGTIPKEIPAMQQLHTQP-EVEPOVQSPAPRPSLQPHPRLDH 360	
Qy	360 RSVQEAVLAVSGLIISPLGLVAGAIALGLWLRLRGKGDKGPKGFLASVTPVDRRGA 419	
Db	361 RDPLEQAVLAVSGLIISPLGLVAGAIALGLWLRLRGKGDKGPKGFLASVTPVDRRGA 420	
Qy	420 PNL 422	
Db	421 PNL 423	
RESULT 6	035228 PRELIMINARY; PRT; 228 AA.	
ID	035228; PRELIMINARY; PRT; 228 AA.	
AC	035228; PRELIMINARY; PRT; 228 AA.	
GN	EBI3 OR EB13.	
DT	01-JAN-1998 (TREMBLrel. 05, Created)	
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)	
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	
DE	Cytokine receptor-like molecule (Epstein-Barr virus induced gene)	
DE	BB13 OR EB13.	
OS	Mus musculus (Mouse).	
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.	
OX	NCBI_TAXID=10090;	
RP	SEQUENCE FROM N.A.	
RA	Nomura H., Yaguchi N., Hanyuu C., Maeda M., Kikuchi Y., Nakata Y.,	

RESULT 9
 ID 057519 PRELIMINARY; PRT; 881 AA.
 AC 057519;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE GP130p_1.
 GN XGP130.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
 OC Xenopodinae: Xenopus.
 NCBI_TAXID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Chen J.; Grace A.; Chien K.R.;
 RT "partial characterization of putative xenopus gp130.";
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 DR AF041845; AAC03531.1; -.
 DR HSSP; P40189; 1BQU.
 DR InterPro; IPR02996; CRIA.
 DR InterPro; IPR003961; FN_I.II.
 DR InterPro; IPR003529; Hemtopoptn_L_F2.
 DR Pfam; PF00041; fn3; 4.
 DR SMART; SM00060; fn3; 1.
 DR PROSITE; PS01353; HEMATopo_REC_L_F2; UNKNOWN_1.
 SQ SEQUENCE 881 AA; 99003 MW; 7DE794D211138AO CRC64;
 Query Match 9.5%; Score 215.5; DB 13; Length 881;
 Best Local Similarity 23.3%; Pred. No. 3.3e-08;
 Matches 61; Conservative 88; Conservative 61; Mismatches 145; Indels 83; Gaps 19;

Query Match 9.3%; Score 211.5; DB 4; Length 422;
 Best Local Similarity 23.7%; Pred. No. 2.7e-08;
 Matches 53; Conservative 53; Mismatches 145; Indels 95; Gaps 19;

Query 7 GLSRVLVAVATALYSASSSPCPQANGPPGVQYGPGRSYKLCC----PGVTAGDPVSWF 60
 Db 30 GAFRAGSGAHTAVLSPQOPTLL-----GSSLATCSYHGDOPGATA-EGLYWT 77
 Query 61 RDGE---PRLLQGPDSGIGHELVLAQAD----STDECTYICOTLDGALGTIVTLQIYYP 112
 Db 78 LNRRLPPELSRVLNAS---TIALALANLNGSRQRSGDNLVCHARDGSILAGSCLIVYGLP 134
 Query 113 PARPV-YCQOADDENFCTWPSQ--TISGLPTRYLSYRKTVLGARSQRSRSPSTGWP 169
 Db 135 PEKPVNICSWSKNDLICRWTFGAHGTFLHTNSLYKLRVYQDNTCEEYHTVGH 194
 Query 170 C-PQDPGLGAARCYVHGAELFSQYRINTEVNPLG-ASTRLDVSLQSILRPDPPOGLRV 226
 Db 195 CHIPKD-----LALFTYEINWEATNLGSARSDVLTDLUUVTTDPPPWHV 243
 Query 227 ESVPGYPRRLRASWTPSPWPCOPHFLL--KFRLQYRAQHPAWSTWP-----AG 275
 Db 244 SRVGGLEOLPSRVWSP--PAKDFLEQAKYQIRYRVEDSYDWKVVIDVSNOTSCRLAG 300
 Query 276 LEVITTDAGVLPHAVRSARDE---LDAGTWSTNS-PEA----- 311
 Db 301 Lk-----PGTVYFVQVRNCNPGLGIYGGKAGIWESENHPTAASTPRSERPGRGGGAGEP 353
 Query 312 -WGTGSTGTKEIP---AWGQH 331
 Db 354 RGGEPSSCPVRRELKQFFGWLKHH 377
 Query 327 WQQLHTQPPVEPOVDSP 343
 Db 323 -----PDIWKKIDSP 332

RESULT 11

Q9UHH5	PRELIMINARY;	PRT;	422 AA.	
ID Q9UHH5;				
AC Q9UHH5;				
DT 01-MAY-2000 (TRMBLrel. 13, Created)				
DT 01-MAY-2000 (TRMBLrel. 13, Last sequence update)				
DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)				
DE Class I cytokine receptor.				
GN ZCYTOS5.				
OS Homo sapiens (Human).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX NCBI_TaxID:9606;				
RN [1]				
SEQUENCE FROM N.A.				
RP RA	SEQUENCE FROM N.A.			
RA Hiroyama T., Iwama A., Nakamura Y., Nakuchi H.; cytokine receptor like molecule 3."				
RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				
RL EMBL; AB00038; BAA9277.1; -.				
DR HSSP; P16471; IBP3.				
DR MGI; MGI:1440030; Crf1.				
DR InterPro; IPR002996; CRIA.				
DR InterPro; IPR002961; FN_III.				
DR Pfam; PF00041; fn3; 2.				
DR SMART; SM00060; FN3; 1.				
KW Receptor; Signal.				
FT SIGNAL	34	POTENTIAL.		
SQ SEQUENCE	425 AA;	46662 MW;	910535C629CA7056 CRC64;	
Query Match	9.28;	Score 209.5.	DB 11;	Length 425;
Best Local Similarity	23.9%;	Pred. No. 3.9e-08;		
Matches	89;	Conservative	53;	Mismatches 138;
DR	Indels	93;	Gaps	18;
Db 17 TALVASSSPCPOAAGPGVQYQGPGRSVKLCC-----PGVTAGDPVSWFRDGEPKLLQG 70				
Db 43 TAVISSQDPTLII-----GSSLQATCSIHDTPGATA-EGLYTWTNG - FRLPS 88				
Qy 71 PDSGLGHELVLIAQADSTDEGT-----YICQTLDAGLGGTVTOLGYPPARPV-VSCQA 122				
Db 89 ELSRLLNTSTLALANLNGSROQSSDNLYCHARDGSILLAGSCLYVGLPPEKPFNNSCWS 148				
Query Match	9.3%;	Score 210.5;	DB 4;	Length 422;
Best Local Similarity	23.7%;	Pred. No. 3.3e-08;		
Matches	91;	Conservative	53;	Mismatches 145;
DR	Indels	95;	Gaps	19;
Db 123 ADYENFSCTRWPSQ-IGSLPTRYLTYSRKTVLGDSDQRSPSPGWP-PODPIGAA 178				
Db 149 RNMKDTCRWTGPAHGFELTFLTNYSKULWYQONTCEHTVPHSCHIPKD----- 203				
Qy 179 RCVVHGAEFWSSOYRINVTEVNPGL-ASTRLDVSLSILRDPDPPQLRVESVPGVPRRLR 237				
Db 204 -----LALEFPTYEIWTEATNLGSGRSRDVLTLDVDDVTTDPPPVYHVSRRGGLEDQLS 257				
Qy 238 ASWTYPASWPCOPPHFL--KFRLOQTPAQHPAWSTVEP-----AGLEVITDAVG 286				
Db 258 VRWVSP--PALKDFLQAKYQIRIVFEDSYDWKVVYDVSNOTSCLRAGLK----- 307				
Qy 287 LPHAVIVVSARF-----LDAGTWSTWSP-PEA-----WGTPSGTGTTIP 321				
Db 308 TVYFVRCNPNGIYSSKKAGIWIENSHPTAASTPSSERPGPGGGCEPRGGEPSSGPVR 367				
Qy 322 KEIP-----AWGQLH 331				
Db 368 RELKQFLGWLKKH 380				
RESULT 13				
Q9GLW3	PRELIMINARY;	PRT;	227 AA.	
ID Q9GLW3				
AC AC				
DT 01-MAR-2001 (TRMBLrel. 16, Created)				
DT 01-MAR-2001 (TRMBLrel. 16, Last sequence update)				
DT 01-DEC-2001 (TRMBLrel. 19, Last annotation update)				
DE Prolactin receptor (Fragment). Ursus maritimus (Polar bear) (Thalarctos maritimus).				
OS Ursus maritimus (Polar bear) (Thalarctos maritimus).				
OC Mammalia; Carnivora; Fissipedii; Ursidae; Ursus.				
OX NCBI_TaxID:29073;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC TISSUE-LIVER;				
RX MEDLINE=20086658; PubMed=10618852;				
RA Howell-Skalla L.A., Bunick D., Bahr J.M.;				
RT Cloning and sequence analysis of the extracellular region of the polar bear (<i>Ursus maritimus</i>) luteinizing hormone receptor (LHR), follicle stimulating hormone receptor (FSHR), and prolactin receptor (PRLR) genes and their expression in the testis of the black bear (<i>Ursus americanus</i>). Mol. Reprod. Dev. 55: 136-145 (2000).				
RL AF169792; AAC10648.1; -.				
DR EMBL; P14787; LAN3.				
RN [1]				
RESULT 12				
Q9JM58	PRELIMINARY;	PRT;	425 AA.	
ID Q9JM58				
AC Q9JM58;				
DT 01-OCT-2000 (TRMBLrel. 15, Created)				
DT 01-OCT-2000 (TRMBLrel. 15, Last sequence update)				
DT 01-MAR-2002 (TRMBLrel. 20, Last annotation update)				
DE Cytokine receptor like molecule 3 precursor.				
GN CRLF1 OR CRM3.				
OS Mus musculus (Mouse).				
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Murinae; Mus.				
OX NCBI_TaxID:10090;				
RN [1]				

DR	InterPro; IPR002996; CRIA.	QY	64 EPKLLQGPDGSGLHELVLIAQADSTDEGYIC-----QTL-----DGALGGTVTQLL 109
DR	InterPro; IPR003961; FN_III.	Db	65 SSEVL----GSKTKLTIVKEFEDAGHYTCRGGEVLSQMLLNNEDGWSTDILKK 119
Pfan;	PF00041; fn3; 1.	QY	110 GYPARRYVVSQOADEY-NFSCTWSPSQISGLPTRYLTSYRKTKTVLGADSQRSPSTGPW 168
KW	SMART; SM00060; FN3; 1.	Db	120 KEPENKNLVTEAKNNSRFRFCW-----LA1STDVKFSVSHRGSSDPQGV 167
Receptor.		QY	
FT	1	Db	
NON_TER	227	Db	
NON_TER	227	Db	
SEQUENCE	227 AA;	Db	
SEQUENCE	26114 MW;	Db	
SEQUENCE	F5E6C5F33B5D5B49 CRC64;	Db	
Query Match	8.4%; Score 192; DB 6; Length 227;	QY	169 PCQDPLGAAACVHGAFFWSQYRINVTEVNPLGASTFLDVS----- 211
Best Local Similarity	27.6%; Pred. No. 4e-07;	Db	
Matches	61; Conservative 31; Mismatches 75; Indels 54; Gaps 12;	Db	168 TCGEATLSAERYKIEQRY-KRYSVQCDNACTPAETLPTIVVDAVHKLYENYISS 226
QY	126 ENFECTWPSQISGLPTRYLTSYRKTKTVLGADSQRSP--STGPWPCPQDPLGAARCVV 182	QY	212 -LQSILRPDPGQPLGRVEVPGVPRRLASWTPASNCQPH-----FLIKERLQYRPAHPA 267
Db	2 ETETCWWKPGEDOGGLPTNTYLTYRKE---GETTHECPDYISSGPNSCYFNK----- 50	Db	227 FFIRDIIKPDPKPNLKKRP-SKTPQQVEVTWYEDPSW-STPHSYFSLTFSVQVGKKKR 284
QY	183 HGAEEFWSOVRINTEVNPLGAST--RULDVSIQSLTRPDPQGLRVES----- 228	QY	268 WSTVPEPAGEEVITDAYAAGLPHAVRVSARDFLDAGTWSWTS 308
Db	1 KHTSIWTWYITITINATNOMGSSSDPDKYVDTY-IVEPDPPVNLTELKQPEDKKPYLW 108	Db	265 SNTLH--VVDKTSVTVICQGAKVSVQARDRYNNSMSEWA 322
QY	229 VPGYPRRL---RASWTVTASWPCQPHFLKFRQYRAQHPWSTVPAGLEE-VITDA 283	RESULT 15	
Db	109 MKYKPPtLVDVRSGW-----LTLQYERLRLKPKPATNET-HFAQOTQFKLSSL 156	Q16354 ID	Q16354 PRELIMINARY; PRRT; 206 AA.
QY	284 VAGLPHAVRVSARDFLDAGTWSWSPERAWGTGSTGTPKEI 324	AC	Q16354; PRELIMINARY; PRRT; 206 AA.
Db	157 YPGQKYLQVRCKP--DHGFWSNEWSPE----SSIQIPNDV 190	DT	01-NOV-1996 (TREMBLrel. 01, Created)
QY	99ET05 ID	DT	01-NOV-1996 (TREMBLrel. 01, Last sequence update)
Q9ET05	99ET05 PRELIMINARY; PRRT; 327 AA.	DE	01-MAR-2002 (TREMBLrel. 20, Last annotation update)
AC	99ET05 AC	OS	Homo sapiens (Human).
DT	01-MAR-2001 (TREMBLrel. 16, Created)	OC	Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606; RN [1]
DT	01-MAR-2001 (TREMBLrel. 16, Last sequence update)	RP	SEQUENCE FROM N.A.
DT	01-MAR-2002 (TREMBLrel. 20, Last annotation update)	RX	MEDLINE-95286597; PubMed=7768908;
DE	Interleukin-12 p40 subunit.	RA	Fuh G., Wells J.A.; "Prolactin receptor antagonists that inhibit the growth of breast cancer cell lines"; J. Biol. Chem. 270:13133-13137(1995).
OS	Marmota monax (Woodchuck).	RT	DR
OC	Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Sciurinae; Marmota.	RL	HSSP; P16471; 1BP3.
OC	Marmota.	DR	InterPro; IP002996; CR1A.
OX	NCBI_TaxID=9995; RN [1]	DR	InterPro; IP003961; FN_III.
RP	SEQUENCE FROM N.A.	DR	InterPro; IP003528; Hemtopoptn_L_F1.
RX	GARCIA-NAVARRO R., BLANCO-Urgoiti B., Berraondo P., SANCHEZ DE LA ROSA R., VALES A., HERRAS-STUBBS S., LASARTE J.J., BORRAS F., RUIZ J., PRIETO J.; "Protection against Woodchuck Hepatitis Virus (WHV) Infection by Gene Gun Immunization with WHV Core and Interleukin-12."; RY. VIREO; AR288519; AAC01023; 1.	DR	PFam; PF00041; fn3; 2.
RA	InterPro; IPR003961; FN_III.	DR	SMART; SM00060; FN3; 1.
RA	InterPro; IPR003520; Hemtopoptn_L_F3.	DR	PROSITE; PS01352; HEMATOPO_REC_L_F1; UNKNOWN_1.
RA	InterPro; IPR003529; Ig_C1.	KW	Receptor.
RT	InterPro; IPR003598; Ig_C2.	FT	NOLTER
RT	InterPro; IPR003006; Ig_MHC.	SQ	SEQUENCE 1 1 23950 MW; CED939781B0804E CRC64;
DR	Pfam; PF00041; fn3; 1.	Query	Match 8.4%; Score 190.5; DB 4; Length 206;
DR	Pfam; PF00047; Ig_C1.	Best Local Similarity 27.8%; Pred. No. 4e-07;	
DR	SMART; SM000409; Ig_C1.	Matches 62; Conservative 27; Mismatches 93; Indels 41; Gaps 11;	
DR	PROSITE; PS01354; HEMATOPO_REC_L_F3; UNKNOWN_1.	QY	112 PPAP-WVSQOADDYENFSCWPSQISGLPTRYLTSYRKTKTVLGADSQRSPSTGPWPC 170
KW	Immunoglobulin domain.	Db	3 PPQPEIIFCRSPNKEFICWRPQTGQPLPNNSLY-----HRGETLMHEC 51
SEQUENCE	327 AA; 37140 MW;	Db	52 PDPLGAAACVYHGAEP--WSOYRINVTEVNPLGAS-TRLDDVSLOSSILRDPPQGLRV 226
SEQUENCE	42782B3559C224DD CRC64;	QY	171 PDPLGAAACVYHGAEP--WVSQOADDYDVTYIVQDPPLILEAV 111
Query Match	8.4%; Score 191; DB 11; Length 327;	Db	52 PDITGGNSCHFGKQTSWMRITYNMVNMNATNQGSSDELYDVTYIVQDPPLILEAV 111
Best Local Similarity	22.3%; Pred. No. 7.6e-07;	QY	227 ESYPGYPER-LRASWTP-----ASWPQPHFLKFRQPAHQPAWSTVEPAG-L 276
Matches	76; Conservative 50; Mismatches 147; Indels 68; Gaps 13;	Db	112 EYKQPEDKPKYLWIKWSPPTLIDLKTGW-----FTLLEIRLKPEKAEEWE-IHFAGQQT 165
QY	12 LIVAVATALYSSASSPCCPQAWGPPGVQY-----GQGRSRVYLCCPGVYTAGGDPVSNFRDG 63	QY	277 EEVYTDIAYAVGLPHAVRVSARDFLDAGTWSW-----PEAW 312
QY	6 LIVISWWSLWLASPLATWEELRNYYVVELDWBHDPTGETVWLT-CDEEEGITWSEQ 64	Db	166 EFKILSLHPGQKLVQVFCKP-DHGFWSAWSPATFIQIPSAN 206

Sat Jan 18 21:53:46 2003

us-09-924-338-2.rspt

Page 9

Search completed: January 17, 2003, 19:39:09
Job time : 45 secs

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Result No.	Score	Query	Match	Length	DB	ID	Description
1	395.5	IIGA_MOUSE	1	460	1	IL6A_MOUSE	P22272 mus musculus
2	392	CNTR_RAT	1	372	1	IL6A_RAT	Q08406 ratus norvegicus
3	390.5	CNTR_HUMAN	1	462	1	IL6A_HUMAN	P22273 ratus norvegicus
4	382	CNTR_CHICK	1	372	1	IL6A_CHICK	P26692 homo sapiens
5	381	CNTR_CHICK	1	362	1	IL6A_CHICK	P31641 gallus gallus
6	360	IIGA_HUMAN	1	468	1	IL6A_HUMAN	P08887 homo sapiens
7	326.5	IIGA_PIG	1	467	1	IL6A_PIG	Q18796 sus scrofa
8	234	PRUR_MEIGA	1	831	1	PRUR_MEIGA	Q91094 meleagris gallopavo
9	221	PRUR_COILLI	1	830	1	PRUR_COILLI	Q90374 columba livia
10	214	PRUR_CHICK	1	831	1	PRUR_CHICK	Q04594 gallus gallus
11	205.5	PRUR_SHEEP	1	581	1	PRUR_SHEEP	Q46561 ovis aries
12	204.5	PRUR_BOVIN	1	581	1	PRUR_BOVIN	Q28172 bos taurus
13	204	PRUR_RABBIT	1	616	1	PRUR_RABBIT	P14787 oryctolagus cuniculus
14	197.5	PRUR_CEREBL	1	581	1	PRUR_CEREBL	Q28235 cervus elaphus
15	190	PRUR_MARMO	1	327	1	PRUR_MARMO	Q61729 marmota monax
16	190	PRUR_SHEEP	1	327	1	PRUR_SHEEP	Q02815 ovis aries
17	189	PRUR_HUMAN	1	622	1	PRUR_HUMAN	P16471 homo sapiens
18	186	NGCA_CHICK	1	1266	1	NGCA_CHICK	Q03696 gallus gallus
19	184	PRUR_BOVIN	1	327	1	PRUR_BOVIN	P146282 bos taurus
20	183	PRUR_CEREBL	1	327	1	PRUR_CEREBL	Q28234 cervus elaphus
21	183	PRUR_RAT	1	610	1	PRUR_RAT	P05710 ratus norvegicus
22	174.5	PRUR_PIG	1	324	1	PRUR_PIG	Q28938 sus scrofa
23	174.5	PRUR_FELICA	1	329	1	PRUR_FELICA	Q02744 felis silvestris
24	174	PRUR_MOUSE	1	608	1	PRUR_MOUSE	Q08501 mus musculus
25	173.5	PRUR_ORIENTI	1	630	1	PRUR_ORIENTI	Q91513 oreochromis
26	166.5	PRUR_HUMAN	1	328	1	PRUR_HUMAN	P29460 homo sapiens
27	166.5	PRUR_MACMU	1	73	1	PRUR_MACMU	P13592 homo sapiens
28	164.5	PRUR_MACMU	1	328	1	PRUR_MACMU	P48095 macaca mulatta
29	164	PRUR_HORSE	1	329	1	PRUR_HORSE	Q9XSG5 equus caballus
30	150	IIGB_HUMAN	1	918	1	IIGB_HUMAN	P40189 homo sapiens
31	148.5	NCA1_BOVIN	1	853	1	NCA1_BOVIN	P1836 bovis taurinus
32	148.5	IIGB_CANFA	1	329	1	IIGB_CANFA	Q28268 canis familiaris
33	148	IIGB_MOUSE	1	335	1	IIGB_MOUSE	P43432 mus musculus

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5
Searched: 112892 seqs, 41476328 residues
Total number of hits satisfying chosen Parameters: 112892
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_40_*

22

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1
IL6A_MOUSE
ID P22272;
AC P22272;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DE Interleukin 6 receptor alpha chain precursor (IL-6R 1).
GN IL6RA OR IL6B.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Batheria; Rodentia; Sciurognathii; Muridae; Murinae; Mus.
OX NCBI_TaxId=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAINC3H; TISSUE=Spleen;
RX MEDLINE=90278354; PubMed=2112585;
RA Sugita T., totsuka T., Saito M., Yamasaki K., Taga T., Hirano T., RA Kishimoto T.;
RT "Functional murine interleukin 6 receptor with the intracisternal A particle gene product at its cytoplasmic domain. Its possible role in plasmacytogenesis." RT
RL J. Exp. Med. 171:2001-2009(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAINC3H; TISSUE=Liver;
RA Philillo M.T., Ciliberto G., Dentte L.;
RL Submitted (JUL-1990) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6 BINDS TO IL-6 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE REACTIONS AND HEMATOPOESES.
CC -1- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.
CC -1- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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DR MGI:105304; I16ra.
 DR InterPro; IPR002996; CR1A.
 DR InterPro; IPR003961; FN_III.
 DR InterPro; IPR00530; Hemipteroptn_L_F3.
 DR InterPro; IPR005006; Ig_MIC.
 DR InterPro; IPR003598; Ig_C2.
 DR Pfam; PF00041; fn3; 1.
 DR SMART; SM00060; FN3; 1.
 DR PROSITE; PS01354; HEMATopo_REC_L_F3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat; Signal.

FT SIGNAL 1 19 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT DOMAIN 20 460 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 20 364 POTENTIAL.
 FT DOMAIN 386 460 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 40 99 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 25 190 BY SIMILARITY.
 FT DISULFID 47 92 BY SIMILARITY.
 FT DISULFID 117 128 BY SIMILARITY.
 FT DISULFID 162 173 BY SIMILARITY.
 FT CARBOHYD 32 32 N-LINKED (GLCNAC . .) (POTENTIAL).
 FT CARBOHYD 55 55 N-LINKED (GLCNAC . .) (POTENTIAL).
 FT CARBOHYD 150 150 N-LINKED (GLCNAC . .) (POTENTIAL).
 FT CONFLICT 374 374 A -> R (IN REF. 2).
 SQ SEQUENCE 460 AA; FB505905DB085254 CRC64;

Query Match 17.4%; Score 395.5; DB 1; Length 460;
 Best Local Similarity 30.7%; Pred. No. 2.4e+20; Indels 91; Gaps 25;
 Matches 145; Conservative 58; Mismatches 178; Signal 1.

QY 1 MESSSSGLSRVLYAVATLAYSASSWPSOGLPTRYLTYSRKTKTIVLGADSQRSPSTGPWPCP-QDPL 175
 Db 2 LTVGCTLLVALAAAPAVLVGS--CRALEVANGTVTSIPLGATVTLICPKEAAGNVTIH 59

QY 59 WFRDGEPKLQGPD-SGLGHEVLIAQADSTDEGTYICOTLDGAIGGTVTQLQGPPPARV 117
 Db 60 WIVGS---QNRWTITGNTLVIDVQSLDTGYLC-SLNDHIVGTVPLLVDPPEEPK 114

QY 118 VSC-QAADYENFSCTWSPOISQGLPTRYLTYSRKTKTIVLGADSQRSPSTGPWPCP-QDPL 175
 Db 115 LSCRKRKNPLVNVAICEWRPSSTSPTKAVLFARKI----INTNGKSDFOVPCQYSQL 168

QY 176 GAACCVVHGAEFWSOYRI-NVTEVNPGLASTRLDV--SLSQSLRPLDPQGVESVYGI 232
 Db 169 KSFSCQVEILLEDKVHVLSVCSKSHNEAFHSIK-MVQDPDPANLVSATPGR 227

QY 233 PRRERASWTPASWPCQPHFLKFRLQYRPAQHAWA-----TVEPAGLEVITDAVG 286
 Db 228 PRWKVSKHQPHEW-PSYLLFLQLR-- PWWSKEFTVLLPVQAQVQVHDAIG 282

QY 287 LPHAVYRSARDFLDAGTNTSWSPWAEGTPSTGPIKEPA---WQGLHTQPEVQPQVDS 343
 Db 283 VKHVVQVQRKGKEELDGQWSESPVTPWIAE-PRTPAGLWNP-TVQSYE--DS- 335

QY 344 APPRPSLQPHRLLHDRC---SVEQAVLA----SLSIGSFLGLVAGAALGW--- 390
 Db 336 -----ANHEDQYESSTEATSVLAPYQOESSSMSLTFL-YAGGSIAFGLLLCV 381

QY 391 ---LRLRGKGKD-----GSPKPGFLASVLPVDRPGAPN 421
 Db 382 FITLRLQWKSEAEKSRTTSPDPPPSLQPKPTFLPHSSGSDN 433

RECORD 2
 ID CNTR_RAT STANDARD; PRT; 372 AA.
 AC 008406;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

DE Ciliary neurotrophic factor receptor alpha precursor (CNTFR alpha).
 GN CNTFR.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathii; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=93152175; PubMed=8381290;
 RA IP N.Y., McClaire J., Barrezueta N.X., Aldrich T.H., Pan L., Li Y., Wigand S.J., Friedman B., Davis S., Yancopoulos G.D.;
 RT "The alpha component of the CNTF receptor is required for signaling and defines potential CNTF targets in the adult and during development.";
 RT Neuron 10:89-102(1993).
 RL RN [2]
 RP SEQUENCE OF 185-277 FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE-Brain;
 RX MEDLINE=93211934; PubMed=8460125;
 RA Clatterbuck R.E., Price D.L., Kolaitis V.E.;
 RT "Ciliary neurotrophic factor prevents retrograde neuronal death in the adult central nervous system";
 RT Proc. Natl. Acad. Sci. U.S.A. 90:2222-2226(1993).
 RL CC -!- FUNCTION: BINDS TO CNTF (GPA). THE ALPHA CHAIN PROVIDES THE RECEPTOR SPECIFICITY.
 CC -!- SUBUNIT: HETERO trIMER OF THE ALPHA CHAIN, LIFR AND GP130.
 CC -!- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.
 CC -!- TISSUE SPECIFICITY: Nervous system.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 CC -!-
 DR EMBL: S54212; AAB25290; 1;
 DR EMBL: S57711; AAB25918; 1;
 DR PIR: A47387; A47387.
 DR InterPro: IPR02996; CRIA.
 DR InterPro: IPR03961; FN_III.
 DR InterPro: IPR03530; Hantopoptn_L_F3.
 DR InterPro: IPR03006; Ig_MHC.
 DR InterPro: IPR003598; Ig_C2.
 DR Pfam: PF00041; fn3; 1.
 DR Pfam: PF00044; fn3; 1.
 DR SMART: SM00060; FN3; 1.
 DR PROSITE: PS01354; HEMATOPO_REC_L_F3; 1.
 DR Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.
 FT SIGNAL 1 20 POTENTIAL.
 FT CHAIN 21 342 CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA.
 FT PROPEP 343 372 REMOVED IN MATURE FORM (POTENTIAL).
 FT DOMAIN 39 96 IG-LIKE C2-TYPE DOMAIN.
 FT DOMAIN 201 302 FIBRONECTIN TYPE-III.
 FT DISULFID 46 89 POTENTIAL.
 FT CARBOHYD 60 60 N-LINKED (GLCNAC . .) (POTENTIAL).
 FT CARBOHYD 70 70 N-LINKED (GLCNAC . .) (POTENTIAL).
 FT CARBOHYD 142 142 N-LINKED (GLCNAC . .) (POTENTIAL).
 FT CARBOHYD 190 190 N-LINKED (GLCNAC . .) (POTENTIAL).
 FT CARBOHYD 261 261 N-LINKED (GLCNAC . .) (POTENTIAL).
 FT LIFTD 342 342 GPI-ANCHOR (POTENTIAL).
 FT CONFLICT 261 261 N -> D (IN REF. 2).
 SQ SEQUENCE 372 AA; 40822 MW; 3B87EE3923FB149 CRC64;

Query Match 392; DB 1; Length 372;
 Best Local Similarity 31.9%; Pred. No. 3.2e-20;

Matches 113; Conservative 49; Mismatches 164; Indels 28; Gaps 12; CC DR M58557; AAA41431.1; -.

Oy 1 MSSSGSGLSLRSLRVVATAVLSASSSPCPOAWGPPGYOYGOFLGRSVKLCCDGVTAQDPVSMF 60 DR FIR; A37986; A377986.

Db 1 MAASYPWACAVLAAAAAYTOKHSQE -APHYQYERIGTDVTLPCCGAAWSDAAVTR 58 DR HSSP; P16411; IBP3.

61 RDGEPKLQLQPDGDSLGHVELVAQADSTDECTYICOTLDG- ALGGTVTQLQGPAPRIVS 119 DR Interpro; IPR002996; CRIA.

DR Interpro; IPR003961; FN_III.

DR Interpro; IPR003530; Hemcopoptn_L_F3.

DR Interpro; IPR003006; Ig_MHC.

DR Interpro; IPR003598; Ig_C2.

DR Pfam; PF00041; fn3; 1.

DR SMART; SM00060; FN3; 1.

DR SMART; SM00048; IgC2_1.

DR PROSITE; PS01354; HEMATopo_REC_L_F3; 1.

Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat; KW Signal.

KW Signal.

FT CHAIN 1 1.9 INTERLEUKIN_6 RECEPTOR ALPHA CHAIN.

FT DOMAIN 20 4.62 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 20 3.64 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 365 4.62 CYTOLAMERIC (POTENTIAL).

FT DOMAIN 40 9.9 IG-LIKE C-TYPE DOMAIN.

FT DISULPID 25 1.90 BY SIMILARITY.

FT DISULPID 47 9.2 BY SIMILARITY.

FT DISULPID 117 1.28 BY SIMILARITY.

FT DISULPID 162 1.73 BY SIMILARITY.

FT CARBOHYD 32 3.2 N-LINED (GICNAC, .) (POTENTIAL).

FT CARBOHYD 55 5.5 N LINKED (GICNAC, .) (POTENTIAL).

FT CARBOHYD 85 8.5 N LINKED (GICNAC, .) (POTENTIAL).

FT CARBOHYD 150 15.0 N LINKED (GICNAC, .) (POTENTIAL).

FT CONFLICT 227 26.1 XPRWLKVSKQDESWPSYLLQFELRYRPWKSX >

RESULT 3 RDPLAGTAGTWSTWSPBWAQGTGSTGTIPKEIWAQGQLHTQPEVQDSDPAPRPS 349 FT SEQUENCE 462 AA: 50398 MW: A4D604CEDC0537D C9064; (TN REF. 1).

IL6A_RAT ID IL6A_RAT STANDARD; PRT; 462 AA.

P22273; DE Interleukin-6 receptor alpha chain precursor (IL-6R 1).

DT 01-FEB-1991 (Rel. 19, Created)

DT 01-FEB-1995 (Rel. 40, Last sequence update)

DT 16-OCT-2001 (Rel. 40, Last annotation update)

OS Rattus norvegicus (Pat).

OC Mammalia; Eutheria; Rodentia; Chordata; Vertebrata; Euteleostomi; Murinae; Rattus.

OX NCBI_TAXID=10116; RN [1]

RP SEQUENCE FROM N.A.

RC STRAN=Fischer 344; TISSUE=Liver;

RC MEDLINE=91060622; PubMed=2174054;

RA Baumann M., Baumann H., Fey G. H.,

RT "Molecular cloning, characterization and functional expression of the rat liver interleukin 6 receptor." RT J. Biol. Chem. 265:19853-19862(1990).

RL [2]

RN RP IDENTIFICATION OF PROBABLE FRAMESHIFT IN 227-261.

RA Gibson T.

RL Unpublished observations (FEB-1995). CC - FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE REACTIONS AND HEMATOPOIESIS.

CC - SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST (BY SIMILARITY).

CC - SUBCELLULAR LOCATION: Type I membrane protein.

CC - DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.

CC - SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC - SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

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CC DR M58557; AAA41431.1; -.

CC DR FIR; A37986; A377986.

CC DR HSSP; P16411; IBP3.

CC DR Interpro; IPR002996; CRIA.

CC DR Interpro; IPR003961; FN_III.

CC DR Interpro; IPR003530; Hemcopoptn_L_F3.

CC DR Interpro; IPR003006; Ig_MHC.

CC DR Interpro; IPR003598; Ig_C2.

CC DR Pfam; PF00041; fn3; 1.

CC DR SMART; SM00060; FN3; 1.

CC DR SMART; SM00048; IgC2_1.

CC DR PROSITE; PS01354; HEMATopo_REC_L_F3; 1.

CC Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat; KW Signal.

CC KW Signal.

CC FT CHAIN 1 1.9 INTERLEUKIN_6 RECEPTOR ALPHA CHAIN.

CC FT DOMAIN 20 4.62 EXTRACELLULAR (POTENTIAL).

CC FT DOMAIN 20 3.64 CYTOPLASMIC (POTENTIAL).

CC FT DOMAIN 365 4.62 CYTOLAMERIC (POTENTIAL).

CC FT DOMAIN 40 9.9 IG-LIKE C-TYPE DOMAIN.

CC FT DISULPID 25 1.90 BY SIMILARITY.

CC FT DISULPID 47 9.2 BY SIMILARITY.

CC FT DISULPID 117 1.28 BY SIMILARITY.

CC FT DISULPID 162 1.73 BY SIMILARITY.

CC FT CARBOHYD 32 3.2 N-LINED (GICNAC, .) (POTENTIAL).

CC FT CARBOHYD 55 5.5 N LINKED (GICNAC, .) (POTENTIAL).

CC FT CARBOHYD 85 8.5 N LINKED (GICNAC, .) (POTENTIAL).

CC FT CARBOHYD 150 15.0 N LINKED (GICNAC, .) (POTENTIAL).

CC FT CONFLICT 227 26.1 XPRWLKVSKQDESWPSYLLQFELRYRPWKSX >

Query Match 17.2% Score 390 5; DB 1; Length 462;

Best Local Similarity 30.8%; Pred. No. 5.2e-20; Mismatches 183; Indels 85; Gaps 25;

Matches 144; Conservative 55; Mismatches 183; Indels 85; Gaps 25;

Qy 1 MSSSGSGLSLRSLRVVAYTALYSISSPQANGPPGYQGPERSVYKCCPGYTAGD--PVS 58

Db 2 LAVGCLLWLLAAPAVALVGS--CRALEVANGTYTSLSPATVNLICPGKEAAGNATH 59

Qy 59 WERDGPKLQLQPD-SGLGLHDVLQADSDTGTICQTDLGALGTTVQDGTGPPARPY 117

Db 60 WYSGS --- QSREWTNTGTNTLVLRQVNQNDTGHYIC-FLDLHLVGTVPLLVDVPEEPK 114

Qy 118 VSC-QADYENFSCTWSPSQISGLPTRYLTSYRKKTVLGADSQRRSRSPSTGPWPCP-QDPL 175

Db 115 LSCFRKNPLNNAFCEWHPSSTPS-PTTKAVMEAKK-----NTTNGKSDFQVPCOYSQQL 168

Qy 176 GAARCVHGAFFWSQYRI-NYEVNEFLGASTRLDVSLOST--LRDPQQGLRVEVPGY 232

Db 169 KSFSCCEVILEGDKYTHIVSCLVANSVG-SRSSHNVFQOSLKMVQDFPANVVRIPGV 227

Qy 233 PRRLRASWTPASWPPQPHFLIKRQYRPAQHWAWS---TVEPAGLEE---VITAVAG 286

Db 228 PRWLKVSKQDESWPSYLLQFELRYRPWKSX >

Qy 287 LPHAVRSARDFLDAGTWSTWSPEAWGTPSTGTIPKEIPAWGQLHTOPEYEPQVDPAPP 346

Db 283 VRHVVQVRGKEBEDF1GQWSKWSPEVYGT-----W--LAEPRTTPAGIGNPT 328

Qy 347 RPSLQPHPRLLDHDR---SVEQAVIA----SIGLSFLGLYVAGALGLW-----390

Db 329 QVSVDYD--NHEDQYSSTEATSYLAPYQGSSSPPLPTF-VAGGSFLGLLCVFI 384

Qy 391 LRLRRGKD-----GSPKGFLASPVIPVDRRGAFN 421

Db 385 LRLKKKKSQAEKESKTTSPPPYPLGPLKTFPL-LVPLLTTPSGSHN 429

CNTFR_HUMAN	STANDARD;	PRT;	372 AA.
P26592; AC			
DT 01-AUG-1992 (Rel. 23, Created)			
DT 01-FEB-1996 (Rel. 33, Last sequence update)			
DE Ciliary neurotrophic factor receptor alpha precursor (CNTFR alpha).			
GN CNTFR.			
OS Homo sapiens (Human).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo;			
COX NCBI_TaxID=9606;			
RN [1]			
SEQUENCE FROM N.A.			
MEDLINE-91289158; PubMed=1648265;			
Davis S., Aldrich T.H., Valenzuela D.M., Wong V., Furth M.E.,			
Squinto S.P., Yancopoulos G.D.;			
"The receptor for ciliary neurotrophic factor.",			
Science 253:59-63(1991).			
[2]			
SEQUENCE FROM N.A.			
MEDLINE-95293367; PubMed=7774913;			
Brannan C.D.M., Rojas E., Le Beau M.M., Espinosa R.,			
McClain J., Maslowski P., IP N.Y., Copeland N.G.,			
Jenkins N.A., Yancopoulos G.D.;			
Genomic organization and chromosomal localization of the human and			
mouse genes encoding the alpha receptor component for ciliary			
neurotrophic factor.",			
Genetics 125:157-163(1995).			
CC -1- FUNCTION: Binds TO CNTFR (GPA). THE ALPHA CHAIN PROVIDES THE			
CC RECEPTOR SPECIFICITY.			
CC -1- SUBUNIT: HEPETROTRIMER OF THE ALPHA CHAIN, LIFR AND GP130.			
CC -1- SUBCELLULAR LOCATION: Attached to the membrane by a GPI-anchor.			
CC -1- TISSUE SPECIFICITY: NERVOUS SYSTEM AND SKELETAL MUSCLE.			
CC -1- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.			
CC -1- SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.			
CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.			
CC			
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CC use by non-profit institutions as long as its content is in no way			
CC modified and this statement is not removed. Usage by and for commercial			
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).			
CC			
EMBL; M73238; AAA3577.1; -			
EMBL; L38052; AAA91337.1; JOINED.			
EMBL; L38053; AAA91337.1; JOINED.			
PIR; A40854; UHUCN.			
Genew; HGNC:2170; CNTFR.			
MM: 118946; -			
InterPro; IPR022996; CRIA.			
InterPro; PR033961; FN_III.			
InterPro; IPR003530; Hemipteroptn_L_F3.			
InterPro; IPR003006; Ig_MHC.			
InterPro; IPR03598; Ig_c2.			
Pfam; PF00041; fn3; 1.			
Pfam; PF00047; ig; 1.			
SMART; SM00060; FN3; 1.			
SMART; SM00408; IgC2; 1.			
PROSITE; PS01354; HEMATopo_REC_L_F3; 1.			
Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.			
W SIGNAL 1 20 POTENTIAL.			
T CHAIN 21 342 CILIARY NEUROTROPHIC FACTOR RECEPTOR			
T ALPHA.			
T PROPEP 343 372 REMOVED IN MATURE FORM (POTENTIAL).			
T DOMAIN 39 96 IG-LIKE C2-TYPE DOMAIN.			
T DISULFID 201 302 FIBRONECTIN TYPE-III.			
T CARBOHYD 46 89 POTENTIAL.			
T N-LINKED (GLCNAC. . .) (POTENTIAL).			
Query Match 12 LVAVATALVASSPCPQAWGPPGVQYGORGSYKLCCPGVTAGDPVSWRIDGEPEPLQGP 71			
Best Local Similarity 16.8%; Score 382; DB 1; Length 372;			
Matches 122; Conservative 47; Mismatches 168; Indels 48; Gaps 15;			
Db 12 VLAAGAAVVAQRHSPOE - APHQYQERLGSVDTLPCTANWDAATWVNGTD--LAP 66			
Qy 72 DSGLGHEVLQAQDSTDGEYTCQTLDG-ALGSTVTLQIGYPARPVYSCQADY-ENFS 129			
Db 67 DLINGSQLVHLGELGHGSGLYAGEFHRSWHLRHQLVHLGPREPVSRSNTYPKGY 126			
Qy 130 CTWSPSQISGLPT-RYLTSYRKTKTVLGDSQRSPSSTGPWPSCPQDPLGARCVVHAEFW 188			
Db 127 CSWH-----LPTPTLPNTNTVTLIGSK-----IMVCBKDPALKNRCHRYMHLF 172			
Qy 189 S -QYRINVTEVNPLGASTRLLDVSLOSTLRPDPPQGLRVESYSPGVYPRRLRASWTYPSW 246			
Db 173 STIKYKVSISYSNALGHNATADEFDTIVKDPDPENVARPVPSNPRLREYTWTQTPSW 232			
Qy 247 PCQPHFLKFLKFRLQYRPAQHPAWSTVEPA-GLEEVITDAGLPHAVRYSARDFLDAGTWS 305			
Db 233 EDPESEPLKFLKFRLQYRPLDQWVLSGTATDAYKEXIYQVAKD-NEIGIWS 291			
Qy 306 TWSPEAWGTPSTGTIPKEIPAGWQLHTQPEVQVQDSPAPPREPSLQPHPRLDHRSVQE 365			
Db 292 DWSSVAHATPTREE-PRHLTEAQ - AAETTTSSTSSLAPP-----PTTKICD----- 336			
Qy 366 VAVLASLGILSFLGLVAGALAIGLWLRLRGKGDSPKPGFLASV 410			
Db 337 -----PGEL-----PGEL-----PGEL-----PGEL-----PGEL-----PGEL----- 354			
RESULT 5			
CNTFR_CHICK STANDARD; PRT; 362 AA.			
ID P51641; AC P51641; DT 01-OCT-1996 (Rel. 34, Created)			
DT 01-OCT-1996 (Rel. 34, Last sequence update)			
DT 15-JUL-1999 (Rel. 38, Last annotation update)			
DE Ciliary neurotrophic factor receptor alpha precursor (CNTFR alpha) (GPAR			
DE Growth promoting activity receptor alpha) (GPA receptor alpha) (GPAR			
GN CNTFR.			
OS Gallus gallus (Chicken).			
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauvia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.			
OC NCBI_TaxID=9031; OX NCBI_SEQUENCE FROM N.A.			
OX MEDLINE=95401882; PubMed=7671828;			
RA Heller S., Finn T.P., Huber J., Nishi R., Geissen M., Pueschel A.W., Rohrer H.;			
RA "Analysis of function and expression of the chick GPA receptor (GPAR alpha) suggests multiple roles in neuronal development.";			
RA Development 12: 269-279 (1995).			
CC -1- FUNCTION: BINDS TO CNTFR (GPA). THE ALPHA CHAIN PROVIDES THE			

CC	-	RECEPTOR SPECIFICITY.	
CC	-	SUBCELLULAR LOCATION: Attached to the membrane by a GPI anchor (By similarity).	
CC	-	TISSUE SPECIFICITY: HIGHLY EXPRESSED IN NERVOUS SYSTEM. ALSO FOUND IN SKELETAL MUSCLE.	
CC	-	SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.	
CC	-	SIMILARITY: CONTAINS 1 FIBRONECTIN TYPE III-LIKE DOMAIN.	
CC	-	SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.	
CC	-	This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).	
CC	-	EMBL; U29245; AAA87838; 1; -;	
DR	DR	EMBL; 248368; CAA88184; 1; -;	
DR	DR	HSSP; P16471; BP3.	
DR	DR	InterPro; IPR01996; CRLA.	
DR	DR	InterPro; IPR03961; Hemopoein_L_F3.	
DR	DR	InterPro; IPR03530; Hemopoein.	
DR	DR	InterPro; IPR03006; Ig_MHC.	
DR	DR	InterPro; IPR033598; Ig_c2.	
Pfam	PF00041; fn3; 1.		
Pfam	PF00007; ig; 1.		
SMART	SM00060; FN3; 1.		
SMART	SM00408; IGC2; 1.		
PROSITE	PS0134; HEMATOPO_REC_L_F3; 1.		
KW	Receptor; GPI-anchor; Glycoprotein; Immunoglobulin domain; Signal.		
FT	SIGNAL 19 POTENTIAL.		
FT	CHAIN 20 334 CILIARY NEUROTROPHIC FACTOR RECEPTOR ALPHA.		
PROPEP	335 362 REMOVED IN MATURE FORM (POTENTIAL).		
FT	DOMAIN 37 94 IG-LIKE C2-TYPE DOMAIN.		
FT	199 300 FIBRONECTIN TYPE-III.		
FT	DISUFID 44 87 POTENTIAL.		
FT	CARBHYD 58 58 N-LINED (GLCNAC. . .) (POTENTIAL).		
FT	CARBHYD 68 68 N-LINED (GLCNAC. . .) (POTENTIAL).		
FT	CARBHYD 140 140 N-LINED (GLCNAC. . .) (POTENTIAL).		
FT	CARBHYD 188 188 N-LINED (GLCNAC. . .) (POTENTIAL).		
FT	LIPID 334 334 GPI-ANCHOR (POTENTIAL).		
FT	CONFFLICT 337 337 A -> V (IN REF 1,2).		
SQ	SEQUENCE 362 AA; 40307 MW; 5A90217EB48419F7 CRC64;		
Query Match	16.7%; Score 381; DB 1; Length 362;		
Best Local Similarity	30.4%; Pred. No. 1.8e-19;		
Matches	53; Mismatches 164; Indels 56; Gaps 16;		
Db	7 SSSCGSLRSVLVAVATALVASSPOPQANGPPGVOYQOPRSVKLCCPGVTAGDGVSWFRF 61		
Db	8 SACCYVLAAYWWVVAQRHSCQDS-----HQYERYADVDTMKGSNDWDRAVTWA 57		
Qy	2 DGEPKLQGPDSLGL-GHELVLAQADSTDETYICOTLDGA---LGTVTQLGYPPPARPY 117		
Qy	3 NG ---TDIDSHUNGSYLLKNDLTQSQYSC-YEGSWHLKRYQTLYRVGPKEPV 111		
Qy	4 118 VSCQQADY-ENFESTWS-PSQISGLPTRYLTSYRKTKVLAGDSQRSPSTGPWICPCPDPL 175		
Db	5 112 LMCRSNNYPGFYCSWHLPS----PTYIIFNSNTSING-----TREMYCEKDIF 157		
Qy	6 176 GAARCVHHGAEEFWs-QYRINTVEVNPLGMASTRLLDVLSOSILRDPPOGLLVEVPGPY 233		
Db	7 158 PKNHCHYVRLQLESTVYKRYTLYVNAKGSKS-----TDETYICOTLDGA---LGTVTQLGYPPPARPY 117		
Db	8 RRLRASWTFYASWPQCPHFLKFRLQYRPQHPAWSTYEP-AGLEEVITDAVAGLPHAYR 292		
Qy	9 234 RLRLYQWNSWSSWPPESEFLKEFFLRPFLILDQWQHVEYSDGTSHTIAYGKEYITC 277		
Db	10 218 RLRLYQWNSWSSWPPESEFLKEFFLRPFLILDQWQHVEYSDGTSHTIAYGKEYITC 277		
Qy	11 293 VSARDFLDAGTWIWSWSPNGTPSTGTIDKEIPAWGQLHNPQEVEPQVQDSSPAPRPSLQP 352		
RESULT 6			
ID	IL6A_HUMAN STANDARD; PRT; 468 AA.		
ID	IL6A_HUMAN		
AC	Q16202;		
DT	01-NOV-1988 (Rel. 09, Created)		
DT	01-NOV-1988 (Rel. 09, Last sequence update)		
DT	16-OCT-2001 (Rel. 40, Last annotation update)		
DE	Interleukin-6 receptor alpha chain precursor (IL-6R alpha) (IL-6R 1)		
DE	CD126 antigen.		
GN	IL6R.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.		
OX			
NCBI_TAXID=9606;			
RN	[1]		
RP	SEQUENCE FROM N.A. (LONG ISOFORM).		
RX	MEDLINE=88035347; PubMed=3136546;		
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B., Taniguchi T., Hirano T., Kishimoto T.; Molecular structure of interleukin-6 receptor. ";		
RA	Proc. Jpn. Acad., B, Phys. Biol. Sci. 64:209-211(1988).		
RT	"Cloning and expression of the human interleukin-6 (BSF-2/IFN beta 2) receptor.";		
RT	Science 241:825-828(1988).		
RN	[2]		
RP	SEQUENCE FROM N.A. (LONG ISOFORM).		
RA	Yamasaki K., Taga T., Hirata Y., Yawata H., Kawanishi Y., Seed B., Taniguchi T., Hirano T., Kishimoto T.; Molecular structure of interleukin-6 receptor. ";		
RA	Proc. Jpn. Acad., B, Phys. Biol. Sci. 64:209-211(1988).		
RN	[3]		
RP	SEQUENCE FROM N.A. (LONG ISOFORM).		
RX	MEDLINE=91316983; PubMed=1872801;		
RA	Schootink H., Stoyan T., Lenz D., Schmitz H., Hirano T.,		
RA	Kishimoto T., Heinrich P.C., Rose-John S.; Molecular structure of interleukin-6 receptor. ";		
RT	"Structural and functional studies on the human hepatic interleukin-6 receptor. Molecular cloning and overexpression in HepG2 cells.";		
RT	Biochem. J. 277:659-664(1991).		
RL			
RN	[4]		
RP	SEQUENCE OF 313-365 FROM N.A. (SHORT ISOFORM).		
RX	MEDLINE=94333499; PubMed=8056053;		
RA	Boriuchi S., Koyanagi Y., Zhou Y., Miyamoto H., Tanaka Y., Waki M., Matsunoto A., Yamamoto M., Yamamoto N.; Soluble interleukin-6 receptors released from T cell or granulocyte/macrophage cell lines and human peripheral blood mononuclear cells are generated through an alternative splicing mechanism. ";		
RT	Proc. J. Immunol. 24:1945-1948(1994).		
RT			
RL			
RN	[5]		
RP	PARTIAL SEQUENCE, CARBOHYDRATE-LINKAGE SITES, AND DISULFIDE BONDS.		
RX	MEDLINE=99167486; PubMed=10066782;		
RA	Cole A.R., Hall N.E., Treutlein H.R., Eddes J.S., Reid G.E., Moritz R.L., Simpson R.J.;		
RA	"Disulfide bond structure and N-glycosylation sites of the extracellular domain of the human interleukin-6 receptor.";		
RT	J. Biol. Chem. 274:7207-7215(1999).		
RT			
RL			
RN	[6]		
RP	MUTAGENESIS.		
RX	MEDLINE=93223711; PubMed=8467812;		
RA	Yawata H., Yasukawa K., Natsuka S., Murakami M., Yamasaki K., Hibi M., Taga T., Kishimoto T.; Structure-function analysis of human IL-6 receptor: dissociation of amino acid residues required for IL-6-binding and for IL-6 signal transduction through gp130. ";		
RA	EMBO J. 12:1705-1712(1993).		
CC	"Function: part of the receptor for interleukin 6. Binds to IL-6 with low affinity, but does not transduce a signal. Signal activation necessitate an association with IL6ST. Activation may		
CC	"		

LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE REACTIONS AND HEMATOPOESIS.

-!- FUNCTION: LOW CONCENTRATION OF A SOLUBLE FORM OF INTERLEUKIN-6

CC RECEPTOR ACTS AS AN AGONIST OF IL-6 ACTIVITY.

CC -!- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R ALPHA AND 2 IL6ST.

CC -!- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN (LONG FORM).

CC SECRETED (SHORT FORM).

CC -!- ALTERNATIVE PRODUCTS: 2 ISOFORMS; A LONG FORM (SHOWN HERE) AND A SHORT FORM; ARE PRODUCED BY ALTERNATIVE SPLICING.

CC -!- TISSUE SPECIFICITY: THE SHORT FORM IS EXPRESSED IN PERIPHERAL BLOOD MONONUCLEAR CELLS AND weakLY FOUND IN URINE AND SERUM.

CC -!- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE N-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.

CC -!- PTM: A SHORT SOLUBLE FORM MAY ALSO BE RELEASED FROM THE MEMBRANE BY PROTEOLYSIS.

CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.

CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -!- DATABASE: NAME-PROW: NONE-CD guide CD126 entry;
WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd126.htm".

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DR EMBL; X12830; CAA31312_1; .

DR EMBL; X58298; CAA41231_1; .

DR EMBL; S72848; AAC00635_1; .

DR PIR; A41242; A41242.

DR PIR; S14621; S14621.

DR PIR; S17468; S17468.

DR PIR; JU0080; JU0080.

DR Genew; HGNC; 6019; IL6R.

DR MIM; 147880; .

InterPro; IPR002996; CRIA.

InterPro; IPR003961; FN_III.

InterPro; IPR003520; Hemtopoptn_L_F3.

InterPro; IPR03006; Ig_MHC.

InterPro; IPR003538; Ig_c2.

Pfam; PF00041; fn3_1.

Pfam; PF00047; ig_1.

DR SMART; SM00050; FN3; 1.

DR PROSITE; PS01354; HEMATopo_REC_L_F3; 1.

KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat; Alternative splicing; Signal.

SIGNAL 1 19

FT CHAIN 20 468 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.

FT DOMAIN 20 365 EXTRACELLULAR (POTENTIAL).

FT DOMAIN 366 386 POTENTIAL.

FT DOMAIN 387 468 CYTOPLASMIC (POTENTIAL).

FT DISULFID 40 103 IG-LIKE C2-TYPE DOMAIN.

FT DISULFID 25 193 SIGNAL 1 19

FT DISULFID 47 96 DISULFID 121 132

FT DISULFID 165 176 N-LINKED (GLCNAC. .);

FT CARBOHYD 55 93 N-LINKED (GLCNAC. .);

FT CARBOHYD 93 93 N-LINKED (GLCNAC. .);

FT CARBOHYD 221 221 N-LINKED (GLCNAC. .);

FT VARSPLIC 356 365 VQSSSVIP -> GSRRGSCGL (IN SHORT ISOFORM).

FT VARSPLIC 366 468 MISSING (IN SHORT ISOFORM).

FT MUTAGEN 121 121 C->S: COMPLETE LOSS OF LIGAND-BINDING.

FT MUTAGEN 122 122 F->A: NO CHANGE OF LIGAND-BINDING.

FT MUTAGEN 132 132 C->A: COMPLETE LOSS OF LIGAND-BINDING.

FT MUTAGEN 134 134 W->L: COMPLETE LOSS OF LIGAND-BINDING.

FT MUTAGEN 140 140 P->G: NO CHANGE OF LIGAND-BINDING AND IL6 SIGNALING.

F->L: NO CHANGE OF LIGAND-BINDING AND IL6 SIGNALING.

C->L: COMPLETE LOSS OF LIGAND-BINDING AND IL6 SIGNALING.

F->L: NO CHANGE OF LIGAND-BINDING SIGNALING.

C->A: COMPLETE LOSS OF LIGAND-BINDING.

D->T: 30% DECREASE OF LIGAND-BINDING AND IL6 SIGNALING.

V->G: 80% DECREASE OF LIGAND-BINDING AND NO IL6 SIGNALING.

C->D: COMPLETE LOSS OF LIGAND-BINDING.

C->A: NO CHANGE OF LIGAND-BINDING AND SIGNALING.

D->V: COMPLETE LOSS OF LIGAND-BINDING.

R->S: 30% DECREASE OF LIGAND-BINDING AND IL6 SIGNALING.

W->Q: 30% DECREASE OF LIGAND-BINDING AND INCREASE OF IL6 SIGNALING.

E->A: 50% DECREASE OF LIGAND-BINDING AND IL6 SIGNALING.

C->D: 30% INCREASE OF LIGAND-BINDING AND 100% INCREASE IN IL6 SIGNALING.

V->P: 50% DECREASE OF LIGAND-BINDING AND 50% INCREASE IN IL6 SIGNALING.

I->D: COMPLETE LOSS OF LIGAND-BINDING.

H->I: NO CHANGE OF LIGAND-BINDING AND IL6 SIGNALING.

D->G: 70% DECREASE OF LIGAND-BINDING AND NO IL6 SIGNALING.

G->P: 80% DECREASE OF LIGAND-BINDING AND NO IL6 SIGNALING.

Q->K: COMPLETE LOSS OF LIGAND-BINDING.

R->G: COMPLETE LOSS OF LIGAND-BINDING.

SEQUENCE 468 AA: 51547 MW: 62AA239FA14F1BBB CRC64;

Query Match 15.8%; Score 360; DB 1; Length 468;

Best Local Similarity 28.4%; Pred No. 6 8e-18;

Matches 129; Conservative 57; Mismatches 196; Indels 72; Gaps 19;

QY 1 MSSSGSGISRSVLYAVATLVYASSSPCPQAWGPVGVOQGPGRSYVKLCPGVTAQGD--FVS 58

Db 2 LAVGCALLAALLAAPGAAL--APRRCPCPQEVARGVPLIPGDSVTLTPGVPEPDNATVH 59

QY 59 WFRDGEPKLQGPD-----SGLGHFLVLQAQDSTDEGTYCQTLDLGALGTETVTLQG 110

Db 60 W-----VLRKAAGAPSRSWRGMGRILLRSYQLHSQNTSCYRA GRPA GTVHLVD 111

QY 111 YPPARPVSC-QADYDENSCTWSPSQSQLGLPTRYLTSYRKTKTVLGADSQRSPSPSTG-PW 168

Db 112 VPPEEPQLCFRKSPLSNVCEMGPRSTSLLT-----KAVLYFKFQNSPAEDQE 163

QY 169 PC---PQDPLGAARCTVYHGAEEFWSOVPIINVTEVNPIGAS-TRLDLVSQSLRLPDPFG 223

Db 164 PCYSQSEQKFQSKQCLAVEEGDS--SFYVSMCVAFFSKSTOTFOFGTQLQDPAN 221

QY 224 LRVESVPYPRRLRASWTPASWPCQPHFLKERLQYRPAQHPAWSYEPAGLEE--VIT 281

Db 222 ITVTAVANPRNPLSVNDPHPSWN-S-SSTYRLRFELRYAERSKTFTWVVKQLQHHCVTH 280

QY 282 DAVAGLPHAVRYSARDFTDAGTWSTWSDEAWGTPSTGTPKEIPAWGGLHTOPEVEPOVD 341

Db 281 DAWSGLRHVQLRAQEESQGEMSETEAMGTPTWTES-----RSPPAENEVS 328

QY 342 SPAPPRLPQPHPLRHDSDYEQAV---LASLGTLISFLGLIVAYAALG----- 388

Db 329 TPMQALTINKDDNNIL-FRDSANATSLVQDSSSVPLFT-VAGGSIAFGTLLCIATVL 386

QY 389 ----LW-LRLRGKGDKSPKPGLASVLPVDRP 417

Db 387 RFKKTWKLRALEKGTSMHPPYPSLQGLVPERPRP 420

IL6A_PIG STANDARD; PRT; 467 AA.
 ID IL6A_PIG
 AC 018796;
 DT 16-Oct-2001 (Rel. 40, Created)
 DT 16-Oct-2001 (Rel. 40, Last sequence update)
 DT 16-Oct-2001 (Rel. 40, Last annotation update)
 DE Interleukin-6 receptor alpha chain precursor (IL-6R-alpha) (IL-6R 1).
 GN IL6R.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 OX NCBI_TAXID=9823;
 RN [1] RP SEQUENCE FROM N.A.
 RA Morris K.R.; Strom A.D.G.;
 RT "Cloning and expression of biologically active porcine IL-6 receptor
 alpha chain.";
 RL submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
 RN [2] RP SEQUENCE OF 123-186 FROM N.A.
 RC TISSUE-Liver;
 RA Klier J.J.; Matteri R.L.;
 RT "Partial cDNA sequence of porcine interleukin 6 receptor.";
 RL Submitted (JUL-1997) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PART OF THE RECEPTOR FOR INTERLEUKIN 6. BINDS TO IL-6
 WITH LOW AFFINITY, BUT DOES NOT TRANSDUCE A SIGNAL. SIGNAL ACTIVATION MAY
 ACTIVATION NECESSITATE AN ASSOCIATION WITH IL6ST. ACTIVATION MAY
 LEAD TO THE REGULATION OF THE IMMUNE RESPONSE, ACUTE-PHASE
 REACTIONS AND HEMATOPOIESIS.
 CC -!- SUBUNIT: HEXAMER OF 2 IL6, 2 IL6R-ALPHA AND 2 IL6ST* (BY
 CC -!- SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: TYPE I membrane protein.
 CC -!- TISSUE SPECIFICITY: EXPRESSED IN LIVER.
 CC -!- DOMAIN: THE TWO FIBRONECTIN TYPE III-LIKE DOMAINS CONTAINED IN THE
 C-TERMINAL PART FORM TOGETHER A CYTOKINE-BINDING DOMAIN.
 CC -!- SIMILARITY: CONTAINS 1 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAIN.
 CC -!- SIMILARITY: CONTAINS 3 FIBRONECTIN TYPE III-LIKE DOMAINS.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
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 or send an email to license@isb-sib.ch).
 CC -!- DR AF147881; AAF73109_1; -;
 DR AF015116; AAB76916_1; -;
 DR IPR02996; CRIA.
 DR InterPro; IPR03530; Hemocoptoptn_L_F3.
 DR InterPro; IPR03006; Ig_MHC.
 DR InterPro; IPR03598; Ig_c2.
 DR Pfam; PF00041; fn3; 19_c2.
 DR SMART; SM00047; ig; 1.
 DR PROSITE; PS01354; HEMATopo_REC_L_F3; 1.
 KW Receptor; Transmembrane; Glycoprotein; Immunoglobulin domain; Repeat;
 KW Signal.
 FT SIGNAL 1 19 BY SIMILARITY.
 FT CHAIN 20 467 INTERLEUKIN-6 RECEPTOR ALPHA CHAIN.
 FT DOMAIN 20 365 EXTRACELLULAR (POTENTIAL).
 FT TRANSMEM 366 386 POTENTIAL.
 FT DOMAIN 387 467 CYTOPLASMIC (POTENTIAL).
 FT DOMAIN 40 103 IG-LIKE C2-TYPE DOMAIN.
 FT DISULFID 25 193 BY SIMILARITY.
 FT DISULFID 47 96 BY SIMILARITY.
 FT DISULFID 121 132 BY SIMILARITY.
 FT DISULFID 165 176 BY SIMILARITY.
 FT CARBOHYD 55 55 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 93 93 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 221 221 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 350 350 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 467 AA; 51066 MW; A2B0B884FF21C02 CRC64;
 Query Match 14.4%; Score 326.5; DB 1; Length 467;
 Best Local Similarity 28.2%; Pred. No. 1, 4e-15;
 Matches 129; Conservative 56; Mismatches 203; Indels 69; Gaps 20;
 QY 12 IVAVATVALSVASSPPCP-QANGPPG-----VOYQOPGRSVKLICPGVYTAGD-PVSW 59
 Db 1 MLAVGGALLPAALLAAGMIALAPRGCCSKLEYAQDVLTSLPGASVTLICPGGGPGDNATIHW 60
 QY 60 FR----DGEPKLQLQGDSGLGHELYLAQADSTDEGYTCQTLDAIGGTVTQLQGYAPP 115
 Db 61 VLRLNOVTGSP---DGRPAGYGRRLJLKSVOIISDGSNYSKYO-DGYVAGSYRLLVDPAPPEE 116
 QY 116 PVVSC-QADDYENFSCTWSPSQISGLPTRLTSYRKKTVLGADSQRSP-STGPWNCPQD 173
 Db 117 PQLSCKRSKSPSLSNVGCEWRP-----RSPSPSPTKAVLLVRFKNSPNVSPEDFOEC-QY 167
 QY 174 PLGAAR-CVYHGAEEFWSOYRI-NYTEVNPLGA-STRLLDVSLOSLIRPDPQGLREV 229
 Db 168 SLEAQREFFCOLAVPDEDNSFHTLVANSQSSTPQIFEGYGLQDPDPVNITVSAV 227
 QY 230 PGYPRLRASMTYPASWPCQPHELLKFRLQYRPAQHPAWSVTPEAGLEE-VITDAVAGL 287
 Db 228 DRNPRLQSVTWDQDPWNSY-FYRLQFELRYAERSKTFTWYMKELQHCTHDWSGM 286
 QY 288 PHAVRYSARDFLDTWSPEAWGTPST---GTPKEPLPAWGGLHTOPEVEPVYDSP 343
 Db 287 RHVVQLQRAQEEFGHGLWSENOEVIGIPWTESRSSPAETEPLSQTADPTYNEDDEISSK 346
 QY 344 APPRPSLQPHRPLLDIRDSVQEQAVALSGLGILSFLGLVAGALGWLRLRGG----K 398
 Db 347 ESANATSLP---VQDASVPLPFTLVAGGLAFGTL---LCIGTLIRFKKTGQLQALK 398
 QY 399 DGS-----PKPGLFLASVLPYDVRGPARN 421
 Db 399 EGKTNMHPYPSLGQLVPERPKSTPVPLSPVSN 435
 RESULT 8
 PRLR_MELGA
 ID PRLR_MELGA STANDARD; PRT; 831 AA.
 AC 091094; Q9J091; Q91022;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1999 (Rel. 38, Last annotation update)
 DE Prolactin receptor precursor (PRL-R) (TPR1R).
 GN PRLR.
 OS Meleagris gallopavo (Common turkey).
 OC Bokarioti; Metazoia; Chordata; Craniata; Vertebrates; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 OX NCBI_TAXID=9103;
 RN [1] RN SEQUENCE FROM N.A.
 RC TISSUE-Kidney;
 RX MEDLINE=97057891; PubMed=8302221;
 RA Zhou J.F., Zadworny D., Ghemeini D., Kuhnlein U.;
 RT Molecular cloning, tissue distribution, and expression of the
 RT prolactin receptor during various reproductive states in Meleagris
 RT gallopavo.
 RT Biol. Reprod. 55:1081-1090(1996).
 RN SEQUENCE OF 82-121 AND 473-522 FROM N.A.
 RC TISSUE-Ovary;
 RA Pitts G.R., You S.K., Foster D.N., el Halawani M.E.;
 RA Submitted (MAR-1995) to the EMBL/GenBank/DDBJ databases.
 RL -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
 CC PROLACTIN.
 CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
 CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC DT 15-JUL-1998 (Rel. 36, Last annotation update)

CC DE Prolectin receptor precursor (PRL-R).

CC GN PRLR.

CC OS Columba livia (Domestic pigeon).

CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Columbidae; Columba.

CC OC NCBI_TaxID=8932;

CC RN [1]

CC RN SEQUENCE FROM N.A.

DR RP CROPSAC;

DR RC TISSUE=CROPSAC;

DR RX MEDLINE=94283267; PubMed=7516866;

DR RA Chen X.; Horsemann N.D.;

DR RT "Cloning, expression, and mutational analysis of the pigeon prolectin receptor." ;

DR RL Endocrinology 135:269-276(1994);

DR CC -1- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE PROLECTIN.

DR CC -1- SUBCELLULAR LOCATION: Type I membrane protein.

DR CC -1- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

DR CC -1- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.

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FT DR EMBL: U07694; AAA20646; 1; - .

FT DR HSSP: P16471; 1BP3.

FT DR InterPro: IPR00396; CRIA.

FT DR InterPro: IPR003528; Hemopotonin_L_F1.

FT DR Pfam: PF00041; fn3; 4.

FT DR SMART: SM00060; FN3; 3.

FT DR PROSITE: PS01352; REC_L_F1; 1.

KW FT Receptor; Transmembrane; Glycoprotein; Signal; Repeat.

FT SIGNAL 1 23

FT CHAIN 24

FT DOMAIN 24 831

FT EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 439 438

FT POTENTIAL.

FT DOMAIN 460 459

FT CYTOPLASMIC (POTENTIAL).

FT DOMAIN 25 831

FT FIBRONECTIN TYPE-III 1.

FT DOMAIN 25 122

FT FIBRONECTIN TYPE-III 2.

FT DOMAIN 123 225

FT FIBRONECTIN TYPE-III 3.

FT DOMAIN 228 325

FT FIBRONECTIN TYPE-III 4.

FT DOMAIN 326 428

FT BY SIMILARITY.

FT DISULFID 75 46

FT BY SIMILARITY.

FT CARBOHYD 91 91

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 100 91

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 112 112

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 132 132

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 262 262

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 303 303

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 315 315

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 335 335

FT N-LINKED (GLCNAC. . .) (POTENTIAL).

SEQUENCE 831 AA; 94394 MW; 220916320F77FAC1 CRC64;

Query Match 10.3%; Score 234; DB 1; Length 831;

Best Local Similarity 29.0%; Pred. No. 6.8e-09;

Matches 80; Conservative 40; Mismatches 106; Indels 50; Gaps 15;

QY 113 PARP-WVSCQAADDYENFCTWSQISQLPRTYLTSRKTKTVLGADSQRSPSTGPWPCP 1.71

Db 28 PGPKIIKCRSLKEETCSWWKPGSDGGLPTNTLFYSK----DSSEEKI----YECP 76

QY 172 Q-DPLGARCVYHG--AEFWQSQRINYEVNPFLGAST---RLLDVSQSLRFDPDPPQGLR 225

Db 77 DYTSGPNSCYFRNNTYNTATNEIGNSNSDPQVYDT--SIOPGSPVNLT 1.34

QY 226 VESVPGVPR----LRSWTPASWPCQPHFLKRLQYPAQHPAWSTVEPAGEE- 278

Do 135 LLET----QRYANIMYLWAKNSPPILLADASSMHLHYELRKPEEEWEIW-PVGVQTQ 188

QY 279 -VITDAVAGLPHAVRVSARDFLDAGTMWSWSEAWGTPSTGTRIPKEIPANGOLHTQEVE 337

Db 189 CKNRLAAGMRVVQV--RCMLDPGENSESSERRILLISGLSPPEKPTIKCRS-PEKE 245

QY 338 -----PQVDSPAPPRLSPQHPLDHRDSEVEQ 366

Db 246 TFTCWWKPGLDGGHPTNYT----LLYSKEEGEEQV 275

QY RESULT 9

PRLR_COILI STANDARD; PRT; 830 AA.

TD PRLR_COILI STANDARD; PRT; 830 AA.

AC Q0374;

DT 01-NOV-1997 (Rel. 35, Created)

DT 01-NOV-1997 (Rel. 35, Last sequence update)

DR Best Local Similarity 29.0%; Pred. No. 5.2e-08;

Matches 67; Conservative 36; Mismatches 90; Indels 38; Gaps 12;

QY 111 YPPARPYVSCQADYENFSCWTSPSQISGLPTRYLTSYRKTKTVLGADSQRSPSTGPWPCP 1.70

Db 27 YPGPKIIKCRSLKEETCSWWKPGSDGGLPTNTLFYSK----DSSEEKI----YEC 75

QY 171 PODPL-GAARCYV- HGAEFNSQYRINTENPLGAST---RLLDVSQSLRFDPDPPQGL 2.24

Db 76 PDYGMSSPNSCYFDKNHTNPRTTYNMANNEIGNSNSDPQYDVVT-SIVQPDAPVNL 1.33

QY 225 RVEVSPGYPRRLRASWY-PASWPQCP-----HFLLKFRLQYRPAQHPAWSTVEPAGL 2.76

RESULT 10

PRLR_CHICK
ID PRLR_CHICK
AC Q04594;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Prolactin receptor precursor (PRL-R) (CBRLP)
GN
OS Gallus gallus (Chicken).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galiiformes; Phasianidae; Phasianinae;
OC
OC NCBI_TaxID=9031;
OX [1]
RN
RP
SEQUENCE FROM N.A.
RC STRAN=White leghorn; TISSUE=Kidney;
MEDLINE9307512; PubMed=1445292;
RA Tanaka M., Maeda K., Okubo T., Nakashima K.;
RT "Double antenna structure of chicken prolactin receptor deduced from
the cDNA sequence.";
RL Biochem. Biophys. Res. Commun. 188:490-496 (1992).
CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE
CC -!- PROLACTIN.
CC -!- SUBCELLULAR LOCATION: Type I membrane protein.
CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.
CC -!- SIMILARITY: CONTAINS 4 FIBRONECTIN TYPE III-LIKE DOMAINS.
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CC or send an email to license@isb-sib.ch).

DR EMBL: D13154; BAA02439.1; -.

DR PIR: JQ1655; JQ1655.

DR HSSP; P16471; IBP3.

DR InterPro; IPR02996; CR1A.

DR InterPro; IPR033961; FN_III.

DR InterPro; IPR03528; Hemocoptoptn_L_F1.

DR Pfam; PF00041; fn3; 4.

DR SMART; SM00060; FN3; 3.

DR PROSITE; PS01352; HEMATOPO_REC_L_F1; 1.

KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat.

FT SIGNAL 1 23 POTENTIAL.

FT CHAIN 24 831 PROLACTIN RECEPTOR.

FT DOMAIN 24 438 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 439 459 POTENTIAL.

FT DOMAIN 460 831 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.

FT DOMAIN 123 225 FIBRONECTIN TYPE-III 2.

FT DOMAIN 228 325 FIBRONECTIN TYPE-III 3.

FT DOMAIN 326 428 FIBRONECTIN TYPE-III 4.

FT DISULFID 36 46 BY SIMILARITY.

FT DISULFID 75 86 BY SIMILARITY.

FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 100 100 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 112 112 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 262 262 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 303 303 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 315 315 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 335 831 AA; 94102 MW; 1C4E7591DCADBE9 CRC64; N-LINKED (GLCNAC. . .) (POTENTIAL).

SQ SEQUENCE 831 AA; 94102 MW; 1C4E7591DCADBE9 CRC64;

Query Match 9.4%; Score 214; DB 1; Length 831;

Best Local Similarity 27.5%; Pred. No. 1.6e-07;

Matches 76; Conservative 42; Mismatches 108; Indels 50; Gaps 15;

Qy 113 PARP-VVSCQADYENFSCTWSPSQSLGLPTRYLTYSRKTKTVALGDSQRRSRSPSTGWPCP 171

Db 28 PGKPKIIRCRLKEKFSCKWPKSGUGLPNTYFLYSK-----DSEEET-----YECP 76

Qy 172 Q-DPLGAACRYVY-HGAEFWNSQRYINTEVNPLGAST--RLLDVLSQSTLRLPDPQGLR 225

Db 77 DYRTSSPNSCYFNKNHSPWTFNTVTATNEIGNSSSDPOYVDV--SIVQPGSSTVNL 134

Qy 226 VESVPYPRR-----LRASTKTPASWPCQPHFLLKFRQLYRPAQFPWSTVEPAGLEE- 278

Db 135 LET-----KRSANIMMLWAKNSPPLADASSNNHLHYELRKPEEKEWETIS-YGVOTO 188

Qy 279 -VITDAVAGLPHAVRYSARDLFDAQTWSWSPMEANTPSTGTIPKEPAWQQLHTOPEVE 337

Db 189 CKINRLNAGHRYVVQV--RCTLDPGFSEWESEHLLIPSGQSPPBKPTIKCRS-PEKE 245

Qy 338 -----POYDSPAPRPSLQSPHPRPLDHRDSVEQY 366

Db 246 TETCWPKGLDGHPNT-----LLYSKEEGEQV 275

RESULT 11

PRLR_SHEEP

ID PRLR_SHEEP STANDARD; PRT; 581 AA.

AC P046561; P79205; 046574; P79203; 046569;

DT 15-JUN-2002 (Rel. 41; Created)

DT 15-JUN-2002 (Rel. 41; Last sequence update)

DT 15-JUN-2002 (Rel. 41; Last annotation update)

DE Prolactin receptor precursor (PRL-R) (OPR).

GN PRLR.

OS Ovis aries (Sheep). Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Gekartiodactyla; Ruminantia; Pecora; Bovidae;

OC Cervidae; Caprinae; Ovis.

OX NCBI_TaxID=9940;

RN [1]

RP SEQUENCE FROM N.A., AND ALTERNATIVE SPlicing.

RC TISSUE-Liver, and Mammary gland;

RX MEDLINE=9801468; PubMed=9143303;

RP SPECIFICITY.

RC STRAIN=Scottish blackface; TISSUE=Anterior pituitary;

RX MEDLINE=99049302; PubMed=983246;

RA Tortonese D.J., Brooks J., Ingleton P.M., McNeilly A.S.;

RT "Detection of prolactin receptor gene expression in the sheep
RT pituitary gland and visualization of the specific translation of the
RT signal in gonadotropins.";

RL Endocrinology 139:5215-5223 (1998).

RN [13]

RP SEQUENCE OF 61-395 FROM N.A., ALTERNATIVE SPlicing, AND TISSUE
SPECIFICITY.

RC TISSUE=Corpus luteum, and Fetal liver;

RA Anthony R.Y., Smith G.W., Duong A., Pratt S.L., Smith M.F.;

RT "Two forms of the prolactin receptor messenger ribonucleic acid are
RT present in ovine fetal liver and adult ovary.";

RL Endocrine 3:291-295 (1995).

CC -!- FUNCTION: This is a receptor for the anterior pituitary hormone
CC prolactin.

CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC -!- ALTERNATIVE PRODUCTS: 3 isoforms; 1/long/L-OPR (shown here),

CC 2/short/S-QPR and 3/soluble; are produced by alternative splicing.
 CC -!- TISSUE SPECIFICITY: Expressed in all tissues examined; liver,
 CC pituitary, adrenal gland, ovary and fetal liver.
 CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

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CC or send an email to license@isb-sib.ch).

CC DR EMBL: AF041257; AAB96795_1;

CC DR EMBL: AF041977; AAB96920_1;

CC DR EMBL: AF041979; AAB97082_1;

CC DR EMBL: AF042358; AAB97744_1;

CC DR EMBL: AF042358; AAB97745_1;

CC DR EMBL: AF041978; AAB97965_1;

CC DR EMBL: Y10578; CAA71597_1;

CC DR EMBL: Y10808; CAAT1/66_1;

CC DR HSSP: PI4787; JAN3;

CC DR InterPro: IPR002996; CRIA.

CC DR InterPro: IPR003961; FN_III_1.

CC DR InterPro: IPR003528; Hentopoptn_L_F1.

CC DR Pfam: PF00041; fn3; 2.

CC DR SMART; SR00060; FN4; 2.

CC DR PROSITE: PS01352; HEMATOPO_REC_L_F1; 1.

CC KW Receptor; Transmembrane; Glycoprotein; Signal; Repeat;

CC KW Alternative splicing.

FT SIGNAL 1 24 POTENTIAL.

FT CHAIN 25 581 PROLACTIN RECEPTOR.

FT DOMAIN 25 237 EXTRACELLULAR (POTENTIAL).

FT TRANSMEM 238 258 POTENTIAL.

FT DOMAIN 259 581 CYTOPLASMIC (POTENTIAL).

FT DOMAIN 25 122 FIBRONECTIN TYPE-III 1.

FT DOMAIN 123 227 FIBRONECTIN TYPE-III 2.

FT DISULFID 36 46 BY SIMILARITY.

FT DISULFID 75 86 BY SIMILARITY.

FT CARBOHYD 59 59 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT VARSPLIC 24 66 GQSPPEKKCRPSKGFETVWEPADGGIPTNTYV

FT YRK > ASLYVPGGKCSVCYTMAYPVGGIPLHMYLVC

FT DQYLLVTS (IN ISOFORM 3).

FT VARSPLIC 67 581 MISSING (IN ISOFORM 3).

FT VARSPLIC 286 296 KGSEELRLR > ISQPSRLVSVF (IN ISOFORM

FT VARSPLIC 297 581 2).

FT VARSPLIC 281 281 MISSING (IN ISOFORM 2).

FT VARSPLIC 387 387 I -> V (IN REF. 1; AAB97743/AAB97744),

FT VARSPLIC 581 AA: 65235 MW; EC5344DE538837A0 CRC64;

FT VARSPLIC 9 28; Score 209.5; DB 1; Length 581;

FT VARSPLIC Best Local Similarity 26.8%; Pred. No. 2.e-07;

FT VARSPLIC Matches 61; Conservative 36; Mismatches 94; Indels 37; Gaps 10;

QY 112 PPAR-VVSCQADYENFSCTWSPSQISGLPLPRLYTSYRKVVLGADSQRRSPTGWPCL 170

DB 27 PSEPKLJKCRPKKEFTCWNWPGAGGLPNNTYTYRK-----GETLHEC 75

QY 171 PDDPLGALARCVYHGAEEF --WQYRINTEVNPLG-ASTRLDVSLSIQLRDPQQGLRV 226

DB 76 PDYKTTGGNNSCFPSKKTSIWWMMVITVA!NOMG!SSDPYVDTYIVEPPVNLT 135

QY 227 ESYPGYPRR--LRASTNTP-----ASWPCCQFHELLKFLRQLYRPAQHWNST-VEPAGLE 277

DB 136 EUKHPEDRPKPYWMKWNPKLTDVKSGW-----FSTIQEIRKPEATDWTHFAPKLQ 190

QY 278 EYITDAVAGLPHAVYRSARDFLDAGTWSTWSBEAWGTPSTGTIPKLP 325

DB 191 LKIFNLYPGOKLYVQTRCKP--DHGYTWEWSSE-----SFYQIPNDFP 231

CC RESULT 12

CC PRLR_BOVIN STANDARD; PRT; 581 AA.

CC ID PR1L_BOVIN ID Q2817; O18880; O46591;

CC AC DT 01-NOV-1997 (Rel. 35, Created)

CC DT 01-NOV-1997 (Rel. 35, Last sequence update)

CC DT 15-JUN-2002 (Rel. 41, Last annotation update)

CC DE Prolactin receptor precursor (PRLR).

CC GN PRLR.

CC OS Bos taurus (Bovine).

CC OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

CC OC Bovidae; Bovinae; Bos.

CC OC NCBI_TaxID:913;

CC OX RN [1]

CC RP SEQUENCE FROM N.A. (LONG ISOFORM).

CC RC TISSUE=Endometrium;

CC MEDLINE=32465019; PubMed=1338725;

CC RA Scott P., Kessler M.A., Schulz L.A.;

CC RT Molecular cloning of the bovine prolactin receptor and distribution

CC of prolactin and growth hormone receptor transcripts in fetal and

CC utero-placental tissues.";

CC RL Mol. Cell. Endocrinol. 89:47-58 (1992).

CC RN [2]

CC RP SEQUENCE FROM N.A. (SHORT ISOFORM), AND TISSUE SPECIFICITY.

CC RC TISSUE=Endometrium;

CC MEDLINE=97375450; PubMed=9231767;

CC RA Schuler L.A., Nagel R.J., Gao J., Horseman N.D., Kessler M.A.;

CC RT "Prolactin receptor heterogeneity in bovine fetal and maternal

CC tissues";

CC RL Endocrinology 138:3187-3194 (1997).

CC RN [3]

CC RP SEQUENCE OF 25-234 FROM N.A., AND SEQUENCE OF 25-33.

CC RC TISSUE=Hammary gland;

CC MEDLINE=9525670; PubMed=7738463;

CC RX Tcheliet A., Staten N.R., Creely D.P., Kriivi G.G., Gertler A.;

CC RT "Extracellular domain of prolactin receptor from bovine mammary gland:

CC expression in Escherichia coli, purification and characterization of

CC its interaction with lactogenic hormones.";

CC RT RL J. Mol. Endocrinol. 144:393-403 (1995).

CC RN [4]

CC RP ALTERNATIVE SPlicing.

CC RX MEDLINE=98001468; PubMed=9343303;

CC RA Bignon C., Binart N., Ormandy C., Schuler L.A., Kelly P.A., Djiane J.;

CC RT "Long and short forms of the ovine prolactin receptor: cDNA cloning

CC and genomic analysis reveal that the two forms arise by different

CC alternative splicing mechanisms in ruminants and in rodents.";

CC RT RL J. Mol. Endocrinol. 10:110-120 (1997).

CC CC -!- FUNCTION: THIS IS A RECEPTOR FOR THE ANTERIOR PITUITARY HORMONE

CC PROLACTIN.

CC CC -!- SUBCELLULAR LOCATION: Type I membrane protein.

CC CC -!- ALTERNATIVE PRODUCTS: 2 isoforms; a long form (shown here)

CC CC and a short form; are produced by alternative splicing.

CC CC -!- TISSUE SPECIFICITY: Expressed in all tissues examined; liver,

CC peripheral blood lymphocytes, endometrium, corpus luteum,

CC intestine, fetal thymus, fetal spleen, fetal liver and fetal

CC brain.

CC CC -!- SIMILARITY: BELONGS TO THE CYTOKINE FAMILY OF RECEPTORS.

CC CC -!- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.

CC CC ---

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CC or send an email to license@isb-sib.ch).

CC DR EMBL; L02549; AAA51417; 1. . .

CC DR EMBL; AF027403; AAB8399; 1. . .

CC DR EMBL; AF042780; AAB9774; 8.1; . . .

CC DR EMBL; AF042780; AAB9774; 7.1; ALT-SEQ.

RT	mammary gland.";
DR	Proc. Natl. Acad. Sci. U.S.A. 86:2112-2116(1989).
DR	IPR002986; CR1A.
DR	InterPro; IPRO003961; FN_III.
DR	InterPro; IPR003528; Hemtopoptn_L_F1.
DR	Pfam; PF0041; fn1; 2.
SMART	SM00050; EN3; 2.
PROSITE	PS01352; HEMATOPO_REC_L_F1; 1.
DR	Receptor; Transmembrane; Glycoprotein; Signal; Repeat; KW
KW	Alternative splicing.
SIGNAL	1 24
FT	PROBABLE.
FT	PROLACTIN RECEPTOR.
FT	EXTRACELLULAR (POTENTIAL).
FT	POTENTIAL.
TRANSEM	238 258
FT	CYTOSOLIC (POTENTIAL).
DOMAIN	259 581
FT	FIBRONECTIN TYPE-III 1.
DOMAIN	259 122
FT	FIBRONECTIN TYPE-III 2.
DISULFID	227 227
FT	BY SIMILARITY.
DISULFID	36 46
FT	N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD	59 59
FT	N-LINKED (GLCNAC. .) (POTENTIAL).
CARBOHYD	132 132
VARSPLIC	286 296
FT	KGRSEELLRA > ISQPSRLYSMF (IN SHORT ISOFORM).
VARSPLIC	297 581
FT	MISSING (IN SHORT ISOFORM).
FT	CONFFLICT 120 120
FT	H > D (IN REF. 3).
CONFFLICT	128 128
FT	E -> D (IN REF. 3).
CONFFLICT	137 137
FT	L -> V (IN REF. 3).
CONFFLICT	141 141
FT	H (IN REF. 3).
CONFFLICT	156 157
FT	MT -> IM (IN REF. 3).
CONFFLICT	186 186
FT	L -> P (IN REF. 3).
SEQUENCE	591 AA; 65153 MW; 7385CD06956EE139 CRC64;
Query Match	9.0%
Best Local Similarity	26.5%
Matches	61; Conservative 36; Mismatches 92; Indels 41; Gaps 11;
Qy	112 PPAPR-VVSCQAADDYENFSCTWSPSQISGLPLRYLTSRKKTVLGADSQRRSSTGWPDC 170
Db	27 PPBKPKLYCRSPKGKEETTCWNEPGADGGPLNNTLVYHE-----GETLHHEC 75
Qy	171 PQDPLGAARCVVHG--AEEFWSDYRINTEVNPLG-ASTRLDVSLSQTLRPPDPOQLRV 226
Db	76 PYKTTGGRNCSYPSKKHTSIWKMYVIVNAIGGISSDPYLIVVTPPEPDANITL 135
Qy	227 ESYVGPYPR--LRAWSWTP-----ASWPCOPHFLKFLRQYPAQHPAWS---TVEPAG 275
Db	136 ELKHPEDDKPKLYMKWSPPTMTDKSGH----EIIQVEIRLKPEKATDWETHETLKOTQ 190
Qy	276 LEFYVITDAVAGLPHAVYRSARDELDAGTWSTNSPEANGTPSTGTIPKIP 325
Db	191 LK--IFNLYPGQKLYVQIRCKP--DHGYWSENSPE----SSTQIPNDFFP 231
RESULT 13	
PRIOR_RABBIT	STANDARD;
ID	PRT; 616 AA.
AC	P14787;
DT	01-APR-1990 (Rel. 14, Created)
DT	01-APR-1990 (Rel. 14, Last sequence update)
DT	15-JUN-2002 (Rel. 41, Last annotation update)
DE	Prolactin receptor precursor (PRL-R).
GN	
OS	Oryctolagus cuniculus (Rabbit).
OC	Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;
OC	Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagidae.
OX	NCBI_TaxID=9886;
RN	SEQUENCE FROM N.A.
RP	TISSUE-Mammary gland;
RC	LINE-89184578; PubMed=2928321;
RA	Edery M., Jolicoeur C., Levy-Meyreis C., Dusantier-Fourt I.,
RA	Perridou B., Boutin J.M., Leueniger L., Kelly P.A., Diane J.;
RT	"Identification and sequence analysis of a second form of prolactin receptor by molecular cloning of complementary DNA from rabbit
RT	[1]
RESULT 14	
PRLR_CEREL	
ID	PRLR_CEREL
AC	Q2835;
DT	01-SEP-1997 (Rel. 35, Created)
PRT;	581 AA.


```

Db    65 SSEVL----GSGKTLTILVKEFEDAGHYTCRR----GEVLSQMLLLHKNEDSTWST 114
Qy   110 ----GPPARPVSCOADE-NFSCTWSPSQISGLPTRVLTSYKKTVLGADSORRSP 163
     | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    115 DILKKKEPENKNLVTCEAKNSGRFTCWW-----LTAISNDVNFSVKSHRGSS 162
Qy   164 STGPWPPEPDQDPLGAACRVHGAEPFWSYRINVTEVNPLGASTRLLDS----- 211
     | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    163 DPGVYTGEATLSAERYKIEQEY - KKYSVQCQEDNACPTAEETLPITVWVDAVHLKYE 221
Qy   212 -----LQSTLRPDPPQGLRYESVPGYPRRLRASWTPASWPCOPH - FLLKFRLQYRP 262
     | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    222 NYISSFFTRDIIKPDPPKNLKMKP - SKTPQQEVTWEPDSW-STPHSYFSLTFSVQVQG 279
Qy   263 AQHPAWSTVEPAGLEEVITDAVAGLPHAVRYSARDFELDAGWSTWS 308
     | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db    280 KKKKRNTLH--VDKTSVTVTCQKGAKVSYQARDYNNSSWEWA 322
     | : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: January 17, 2003, 19:38:22

Job time : 18 secs

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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:37:20 ; Search time 22 Seconds
 (without alignments)
 1844.033 Million cell updates/sec

Title: US-09-924-338-2

Perfect score: 2275

Sequence: 1 MSSSSCGLSRVLVAVATALV.....KPGFLASVIPVDRPGAPNL 422

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283224 seqs, 96134422 residues

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%

Listing first 45 summaries

Database : PIR_73;*

1: pir1;*

2: pir2;*

3: pir3;*

4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Description
	%	Length	ID
1	2275	100.0	422 2 I37891
2	1897	83.4	interleukin-11 receptor alpha chain - human
3	395.5	17.4	C; Species: Homo sapiens (man)
4	392	17.2	C; Date: 29-May-1998 # sequence_revision 29-May-1998 # text_change 03-Dec-1999
5	389.5	17.1	C; Accession: I37891; GO1970; GO1971
6	380	16.7	R;Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; Minviell
7	379	16.7	Blood 86, 2534-2540, 1995
8	360	15.8	A; Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic growth factor
9	298.5	13.1	A; Reference number: I37891; MUID:95399754; PMID:7670098
10	221	9.7	A; Accession: I37891
11	214	9.4	A; Status: Preliminary; translated from GB/EMBL/DBBJ
12	204.5	9.0	A; Molecule type: mRNA
13	204	9.0	A; Residues: 1-422 <RES>
14	189	8.3	A; Cross-references: EMBL:238102; NID:9995653; PIDN:CAA86224.1; PID:9995654
15	189	8.3	R;Van Leeuven, F.
16	189	8.3	A; Status: preliminary; translated from GB/EMBL/DBBJ
17	186	8.2	R;Van Leeuven, F.
18	183	8.0	A; Status: preliminary; translated from GB/EMBL/DBBJ
19	183	8.0	A; Cross-references: EMBL:U32323; NID:9975334; PIDN:AAB36491.1; PID:9975335
20	183	8.0	A; Residues: 1-422 <VN>
21	183	8.0	A; Status: preliminary; translated from GB/EMBL/DBBJ
22	174	7.6	R;Van Leeuven, F.
23	174	7.6	A; Status: preliminary; translated from GB/EMBL/DBBJ
24	174	7.6	A; Status: preliminary; translated from GB/EMBL/DBBJ
25	173.5	7.6	A; Status: preliminary; translated from GB/EMBL/DBBJ
26	167.5	7.4	A; Status: preliminary; translated from GB/EMBL/DBBJ
27	166.5	7.3	A; Status: preliminary; translated from GB/EMBL/DBBJ
28	150	6.6	A; Status: preliminary; translated from GB/EMBL/DBBJ
29	149.5	6.6	A; Status: preliminary; translated from GB/EMBL/DBBJ

ALIGNMENTS

RESULT 1	I37891	interleukin-11 receptor alpha chain - human
	C; Species: Homo sapiens (man)	C; Species: Homo sapiens (man)
	C; Date: 29-May-1998 # sequence_revision 29-May-1998 # text_change 03-Dec-1999	C; Date: 29-May-1998 # sequence_revision 29-May-1998 # text_change 03-Dec-1999
	C; Accession: I37891; GO1970; GO1971	C; Accession: I37891; GO1970; GO1971
	R;Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; Minviell	R;Cherel, M.; Sorel, M.; Lebeau, B.; Dubois, S.; Moreau, J.F.; Bataille, R.; Minviell
	Blood 86, 2534-2540, 1995	Blood 86, 2534-2540, 1995
	A; Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic growth factor	A; Title: Molecular cloning of two isoforms of a receptor for the human hematopoietic growth factor
	A; Reference number: I37891; MUID:95399754; PMID:7670098	A; Reference number: I37891; MUID:95399754; PMID:7670098
	A; Accession: I37891	A; Accession: I37891
	A; Status: preliminary; translated from GB/EMBL/DBBJ	A; Status: preliminary; translated from GB/EMBL/DBBJ
	A; Molecule type: mRNA	A; Molecule type: mRNA
	A; Residues: 1-422 <RES>	A; Residues: 1-422 <RES>
	A; Cross-references: EMBL:238102; NID:9995653; PIDN:CAA86224.1; PID:9995654	A; Cross-references: EMBL:238102; NID:9995653; PIDN:CAA86224.1; PID:9995654
	R;Van Leeuven, F.	R;Van Leeuven, F.
	submitted to the EMBL Data Library, July 1995	submitted to the EMBL Data Library, July 1995
	A; Reference number: G08959	A; Reference number: G08959
	A; Accession: G01970	A; Accession: G01970
	A; Status: preliminary; translated from GB/EMBL/DBBJ	A; Status: preliminary; translated from GB/EMBL/DBBJ
	A; Molecule type: DNA	A; Molecule type: DNA
	A; Residues: 1-422 <VN>	A; Residues: 1-422 <VN>
	A; Cross-references: EMBL:U32323; NID:9975334; PIDN:AAB36491.1; PID:9975335	A; Cross-references: EMBL:U32323; NID:9975334; PIDN:AAB36491.1; PID:9975335
	R;Van Leeuven, F.	R;Van Leeuven, F.
	submitted to the EMBL Data Library, July 1995	submitted to the EMBL Data Library, July 1995
	A; Reference number: G08961	A; Reference number: G08961
	A; Accession: G01971	A; Accession: G01971
	A; Status: preliminary; translated from GB/EMBL/DBBJ	A; Status: preliminary; translated from GB/EMBL/DBBJ
	A; Molecule type: mRNA	A; Molecule type: mRNA
	A; Residues: 1-422 <VA2>	A; Residues: 1-422 <VA2>
	A; Cross-references: EMBL:U32324; NID:9975336; PIDN:AAB36492.1; PID:9975337	A; Cross-references: EMBL:U32324; NID:9975336; PIDN:AAB36492.1; PID:9975337
	C; GenBank:	C; GenBank:
	A; Introns: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1; 270/3; 318/1; 358/1; 418/1	A; Introns: 34/1; 54/2; 111/1; 149/2; 160/2; 216/1; 270/3; 318/1; 358/1; 418/1
	C; Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology <CR>	C; Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology <CR>
	F;120-110/Domain: cytokine receptor homology <CR>	F;120-110/Domain: cytokine receptor homology <CR>
	Query Match	Score 100.0%; Score 100.0%;
	Best Local Similarity	Length 422; Best Local Similarity 100.0%;
	Matches 422;	Length 422; Best Local Similarity 100.0%;
	Conservative 0;	Conservative 0;
	Mismatches 0;	Mismatches 0;
	Indels 0;	Indels 0;
	Gaps 0;	Gaps 0;
Qy	1 MSSSCSGLSRVLVAVATALVASSSPCPAQWGPVGQYQGPGRSVKLCPGVTAGDPVSWF	1 MSSSCSGLSRVLVAVATALVASSSPCPAQWGPVGQYQGPGRSVKLCPGVTAGDPVSWF
	Db	1 MSSSCSGLSRVLVAVATALVASSSPCPAQWGPVGQYQGPGRSVKLCPGVTAGDPVSWF
	Qy	61 RDGEPKLLQGPDSGLGHLYVLAQADSTDEGTYICQTLGALGGTWTQLQGYPPAREPVSC
	Db	61 RDGEPKLLQGPDSGLGHLYVLAQADSTDEGTYICQTLGALGGTWTQLQGYPPAREPVSC
	Qy	121 QAADYENFSCKWSPSQISGLPTRYLTYSRKTKTVLGDSQRSPSTGPWPQCDPQDPLGARC
	Db	121 QAADYENFSCKWSPSQISGLPTRYLTYSRKTKTVLGDSQRSPSTGPWPQCDPQDPLGARC

Qy	287	LPHAVRSARDLFAGTWSPEAWGTPSTGTIPKEIPA--WGQLHTQPEVEPVQVDSP	343	RESULT 5
Db	283	VKHYVQVREKEELDQGOMSWPSWVPTGPWIAE-PRTTAGLILWNP--TQVSVE--DS-	335	interleukin-6 receptor precursor (clone lambda P1) - mouse
C;Species:	Mus musculus (house mouse)			
C;Accession:	JL0144			
C;Title:	Functional murine interleukin 6 receptor with the intracisternal a particle			
A;Reference number:	JL0144; MUID:90278354; PMID:2112585			
A;Status:	nucleic acid sequence not shown			
A;Molecule type:	mRNA			
A;Residues:	1-440 <SUG>			
A;Cross-references:	GB:X51976; NID:953548; PIDN:CAA36238.1; PID:953549			
C;Superfamily:	ciliary neurotrophic factor receptor; cytokine receptor homology: immu			
C;Keywords:	cytokine receptor; transmembrane protein			
F;1-19/Domain:	signal sequence #status predicted <SIG>			
F;20-44/Domain:	Interleukin 6 receptor #status predicted <MAT>			
F;45-94/Domain:	immunoglobulin homology <IMM>			
F;117-306/Domain:	cytokine receptor homology <CRS>			
F;358-385/Domain:	transmembrane #status predicted <TRA>			
Query Match	17.1%	Score 389.5; DB 2; Length 440;		
Best Local Similarity	32.3%	Pred. No. 1.4e-18;		
Matches	135;	Conservative 54; Mismatches 162; Indels 67; Gaps 23;		
Qy	1	MSSSCGLSRVLYAVATALVASSPCPQAWGPPCVQGOPGRSVKLCPGVTAQDPVS--	58	
Db	2	LTVGCTLLYVAAAPAVALVLSG--CRALEAVANTVSLPGATVTLCPGEKEAGNTVH	59	
Qy	59	WFEDGPKLUQGPD-SGIGHELVAQAQDSTDEGYICOTLDGAUJLQGYPARPV 117		
Db	60	WVYSGS---QNRENTITGNTLVLRDQLSDTDGYLC-SLNDHLVGTPLLVDPPEPK 114		
Qy	118	VSC-QAADYENFSTWSPOISGLPTRYLTSYRKTKTIVLGADSQRSPSSTGPWPSCP-QDPL 175		
Db	115	LSCFRKNPVLNAICEWRPSSTS-PTKAVLFARKI----NTNGKSDEQVPCQYSQOL 168		
Qy	176	GAACRCVHGAEFWQYRI-NVTEVNPLGASTRLDV--SIQSILRDPDQGLRVESTVQY 232		
Db	169	KSFSCSQVTEILEGDVYHVTSCLVANSVGKSSHNEAFHSLSK-MVQDPDPAFLVVAIPR 227		
Qy	233	PRLRASWTPASWCPQPHFLKPLRQYRPAQHDWS----TVEPAGLEEVITDAVAG 286		
Db	228	PRWLKVSMQHPETWD-PSYLLQQPLQRYR----PVWWSKEFTVLLPVQYQCVTHDALRG 282		
Qy	287	LPHAVRVSARDFELDAGTWSTWSPEAWGTPSTGTIPKEITA---WGQLHTQPEVEPVQVDSP 343		
Db	283	VKHVQVRKEELDQWSEWSPEVGTPIWIAE-PTTPAGLWNP--TQVSVE--DS- 335		
Qy	344	APPRLPSLQHPRLLDHD---SVEQAVALA----SUGILSPLGIGVAGALAGLWL 391		
Db	336	-----ANHEDOYESSTEATSVLAPYQESSSMSLPTFL-VAGGSLAFLGLL 379		
RESULT 6				
S60614				
C;Species:	Gallus gallus (chicken)			
C;Date:	27-Apr-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000			
C;Accession:	S60614			
R;Heiler, S.; Finn, T.P.; Huber, J.; Nishi, R.; Geissen, M.; Pueschel, A.W.; Rohrer, A;Title:	Analysis of function and expression of the chick GPA receptor (GPalpha1) su			
A;Reference number:	S60614; MUID:5401882; PMID:7671828			
A;Accession:	S60614			
A;Status:	preliminary; nucleic acid sequence not shown			
A;Molecule type:	mRNA			
A;Residues:	1-362 <HEL>			
A;Cross-references:	EMBL:Z48168; NID:9971417; PIDN:CAA88184.1; PID:93063774			
C;Superfamily:	ciliary neurotrophic factor receptor			
C;Keywords:	growth factor receptor			

F;2-89/Domain: immunoglobulin homology <IMM>
E;114-294/Domain: cytokine receptor homology <CRS>

Query Match	Score	Length	Best Local Similarity	Pred. No.	Length	Best Local Similarity	Score	Length
Matches 119; Conservative 53; Mismatches 164; Indels 56; Gaps 16;	16.7%	362;	DB 2;	4.8e-18;	380;	DB 2;	379;	DB 1;
Qy 2 SSSCGGLSRVIVAYATALYASSSPCPQANGPVGQYQGPGRSYKLCCPEVTAQDPVSMER 61	16:		Qy 12 LVAVATLVASSSPCPOANGPVGQYQGPGRSYKLCCPEVTAQDPVSMER 61	16:		Qy 12 LVAVATLVASSSPCPOANGPVGQYQGPGRSYKLCCPEVTAQDPVSMER 61	16.7%	372;
Db 7 SACCYVLAAYVYYAQRHQSODS-----HICQERYGADYTMKCCSMDWDAVITWA 57			Db 12 VLAAAAVYYAQRHQSODS-----HICQERYGADYTMKCCSMDWDAVITWA 57			Db 12 VLAAAAVYYAQRHQSODS-----HICQERYGADYTMKCCSMDWDAVITWA 57	30.1%	Pred. No. 5.7e-18;
Qy 62 DGEPKLQLQDPSGL_GHELYLAQADSTDEGTYCQTLDCG---LGITVILQOLGGYPARPV 117			Qy 72 DSGGHLVLAQADSTDEGTYCQTLDCG---LGITVILQOLGGYPARPV 117			Qy 72 DSGGHLVLAQADSTDEGTYCQTLDCG---LGITVILQOLGGYPARPV 117	129	#text_change 21-Jul-2000
Db 58 NG----TDIDSHLNGSYLILKVNVDLTSQGQYSC---YEWSWHIJKYQYLRLGVPPKEBV 111			Db 67 DLLGSQLVLHGGLGEHGSLYACFHRSWHLRQHVLVGLGPPREPVSRSNTYPKGY 126			Db 67 DLLGSQLVLHGGLGEHGSLYACFHRSWHLRQHVLVGLGPPREPVSRSNTYPKGY 126		
Qy 118 VSCQADY-ENFSCTWS-PSQISGLPTRLTYSRKKTVLGAQDSQRSSBSTMGPQDPL 175			Qy 130 CTWSPSQISGLPTRLTYSRKKTVLGAQDSQRSSBSTMGPQDPLGARCVHGAFFW 188			Qy 130 CTWSPSQISGLPTRLTYSRKKTVLGAQDSQRSSBSTMGPQDPLGARCVHGAFFW 188		
Db 112 LMCRSNNYPKGFTCPSWHLPS----PTVTPNSPNISVTHG-----TRENYCERDF 157			Db 127 CSWH-----LPTPTYIPTNTVTLVHSKK-----IMVCEKDPAKNRCHTRMLF 172			Db 127 CSWH-----LPTPTYIPTNTVTLVHSKK-----IMVCEKDPAKNRCHTRMLF 172		
Qy 176 GAACVVHGAEFNS--QYRINTEVNPLGASTRLLDVSLSLRPDPQQGLRVEVPVSPY 233			Qy 189 S--QYRINTEVNPLGASTRLLDVSLSLRPDPQQGLRVEVPVSPY 246			Qy 189 S--QYRINTEVNPLGASTRLLDVSLSLRPDPQQGLRVEVPVSPY 246		
Db 158 PKNICHIRYLQLFETVKVTKYTNALGNKNTLTDEFAYKPDPEPSVAKPVNNP 217			Db 173 STIKYKVTSISVNAKGHNATAITFDEFTIVKPDPEPVNTPRLEVWQTPTW 232			Db 173 STIKYKVTSISVNAKGHNATAITFDEFTIVKPDPEPVNTPRLEVWQTPTW 232		
Qy 234 RRLASWTPASWPQCPHFLKLRLRPAQHPAWSTVPEA-CLEEVEITDVAGLPHAVR 292			Qy 247 PCOPHFLKFRFLQYRPAQHPAWSTVPEA-CLEEVEITDVAGLPHAVR 305			Qy 247 PCOPHFLKFRFLQYRPAQHPAWSTVPEA-CLEEVEITDVAGLPHAVR 305		
Db 218 RLVEYSWQNPSNVPDSEPFPLKEFLRPLLIDQWQHVLELSQTSHTTDAVKEYLIQ 277			Db 233 PDPESFPKFFLRYPLLDQHNLQHEDGTAHTITDQYAGEKYYIQAQKD-NEIGTWS 291			Db 233 PDPESFPKFFLRYPLLDQHNLQHEDGTAHTITDQYAGEKYYIQAQKD-NEIGTWS 291		
Qy 293 VSARDFDAGTWSTWSPEAWGTPSTGTIPKEIAPWGLHOTPEVERQVDSAPPAPPSLQP 352			Qy 306 TWSPEANCTPSTGTIPKEIAPWGLHOTPEVERQVDSAPPAPPSLQP 355			Qy 306 TWSPEANCTPSTGTIPKEIAPWGLHOTPEVERQVDSAPPAPPSLQP 355		
Db 278 VAAKD-NDIGTWSDWVAHATPWTEE-PKHLTT--EVQITETTSTSTSSFPHP----P 328			Db 292 DRSVAIAITPWTEE-PKHLTT--EVQITETTSTSTSSFPHP----P 328			Db 292 DRSVAIAITPWTEE-PKHLTT--EVQITETTSTSTSSFPHP----P 328		#text_change 21-Jul-2000
Qy 353 HPRLLDHRSDEQVAVA-----VLAISLGL 375			Qy 366 VAVLASLGILSFLGLVAGLALGLWLRLRGGRDGSPRPGLASV 4.0			Qy 366 VAVLASLGILSFLGLVAGLALGLWLRLRGGRDGSPRPGLASV 4.0		
Db 329 TTKICDKGAVGVSAGAVAVCWTLAYGV 360			Db 337 -----EGEL-----GSGGGFCAPFLVSV 354			Db 337 -----EGEL-----GSGGGFCAPFLVSV 354		

RESULT 8

A41242

Interleukin-6 receptor precursor - human

N:Contains: interleukin-6 receptor, soluble form

C:Species: Homo sapiens (man)

C:Accession: A41242; sequence_31-Dec-1992 #text_change 21-Jul-2000

R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Seed, B.; Taniguchi, R; Davis, S.; Aldrich, T.H.; Valenzuela, D.M.; Wong, V.; Furth, M.B.; Squinto, S.P.; Yanc

A;Title: Cloning and expression of the human interleukin-6 (BSF-2/IFNbeta 2) receptor

A;Reference number: A41242; PMID:88305347; PMID:3136546

A;Accession number: A41242; PMID:3136546

A;Molecule type: mRNA

A;Residues: 1-48 <YAM>

A;Cross-references: GB: M0566; NID: 933845; PID: CAA31312.1; PMID:933846

R:Yamasaki, K.; Taga, T.; Hirata, Y.; Yawata, H.; Seed, B.; Taniguchi, R; Novick, D.; Engelmann, H.; Wallach, D.; Rubinstein, M.

J. Exp. Med. 170, 1409-1414, 1989

A;Title: Soluble cytokine receptors are present in normal human urine

A;Reference number: A61459; PMID:90010793; PMID:2529343

A;Accession: A61459

A;Molecule type: protein

A;Residues: 20-49 <NOV>

C;Comment: Through this receptor, interleukin-6 induces proliferation, activation, an

RESULT 7

UHICUN

ciliary neurotrophic factor receptor alpha precursor - human

N:Alternate names: CNTR receptor

C:Species: Homo sapiens (man)

C:Accession: A40854; A56526

R:Valenzuela, D.M.; Rojas, E.; Le Beau, M.M.; Espinosa III, R.; Brannan, C.I.; McClain, Genomics 25, 157-163, 1995

A;Title: Genomic organization and chromosomal localization of the human and mouse genes

A;Reference number: A56526; PMID:7774913

A;Accession: A40854; PMID:91289158; PMID:1648265

A;Molecule type: DNA

A;Residues: 1-372 <DAV>

A;Cross-references: GB: M73238

R:Valenzuela, D.M.; Rojas, E.; Le Beau, M.M.; Espinosa III, R.; Brannan, C.I.; McClain, Genomics 25, 157-163, 1995

A;Title: The CNTR receptor sequence appears to contain several PEST regions.

A;Gene: GDB:CNTR

A;Cross-references: GDB:134652; OMIM:118946

A;Map position: 9p13.9p13

C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunog

C;Keywords: glycoprotein; growth factor receptor; membrane protein; phosphatidylinositol

F;2-21/372/Produkt: ciliary neurotrophic factor receptor #status predicted <SIG>

F;39-91/Domain: immunoglobulin homology <IMM>

F;46-89/Disulfide bonds: #status predicted covalent homology <CRS>

F;60,70,142,190/Binding site: carbohydrate (Asn) (covalent) #status predicted

A;Accession: A61459

A;Molecule type: protein

A;Residues: 20-49 <NOV>

C;Comment: Through this receptor, interleukin-6 induces proliferation, activation, an

C;Comment: This growth factor receptor does not have a tyrosine kinase domain.

C;Genetics:

A;Gene: GRB:IL6R

A;Cross-references: GDB:127966; OMIM:147880

A;Mol pos: 1q21-1q21

C;Superfamily: ciliary neurotrophic factor receptor; cytokine receptor homology; immunoglobulin

C;Keywords: acute phase; cytokine receptor; glycoprotein; transmembrane protein

F;1-19/Domain: signal peptide; #status predicted <SIG>

F;20-468/Domain: interleukin 6 receptor #status predicted <MAT>

F;20-363/Domain: extracellular #status predicted <EXT>

F;40-98/Domain: immunoglobulin homology <IMM>

F;121-309/Domain: cytokine receptor homology <CRS>

F;364-386/Domain: transmembrane #status predicted <TMM>

F;387-468/Domain: intracellular #status predicted <INT>

F;47-96/Disulfide bonds: #status predicted

F;55,93,221,245,350/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 15.8%; Score 360; DB 1; Length 468;

Best Local Similarity 28.4%; Pred. No. 1.3e-16; Indels 72; Gaps 19;

Matches 129; Conservative 57; Mismatches 196; Indels 72; Gaps 19;

F;20-462/Domain: interleukin-6 receptor #status predicted <MAT>

F;20-362/Domain: extracellular #status predicted <EXT>

F;40-94/Domain: immunoglobulin homology <IMM>

F;117-306/Domain: cytokine receptor homology <CRS>

F;363-385/Domain: transmembrane #status predicted <TMM>

F;386-462/Domain: intracellular #status predicted <INT>

F;47-92/Disulfide bonds: #status predicted

Query Match 13.1%; Score 298.5; DB 1; Length 462;

Best Local Similarity 27.2%; Pred. No. 1.6e-12; Indels 132; Gaps 25;

Matches 181; Conservative 50; Mismatches 181; Indels 123; Gaps 25;

Db 1 MSSSCGSLSRVIVAVATALYSASSPCPQAWGPPGVQYGPGRSVKLCCPGVTAGD-pvs 58

Qy 1 WFRDGEPKLQLQGPD-SGLGHELVLAQADSTDEGTYICQTLGAGGFTVLQLGYPPARPV 117

Db 2 LAVGTTLLVLLAAPPALVLYGS--CRALEYANGTISUPGATYLICPGKEAGNATH 59

Qy 2 LAVGTTLLVLLAAPPALVLYGS--CRALEYANGTISUPGATYLICPGKEAGNATH 59

Db 360 WVYSGS---QSREWTGTTGNTLVLRQVYNNDTGHYLC-FLDLHLVGTPLVDVPPPEPK 114

Qy 360 VSC-QADYENFSCTWSPSOISGLPTRYLSYRKTVLQGDSSRSRSPSTGPWMPCP-QDPL 175

Db 361 LSCFRKPNLVAECEWHPSSTS-PTTKAVMAFKKI----NFTNGKSDFQVPQYSQQL 168

Qy 361 LSCFRKPNLVAECEWHPSSTS-PTTKAVMAFKKI----NFTNGKSDFQVPQYSQQL 168

Db 362 KSFSEVELELEGDKVYHVSLSKVANSGV-SRSSINVFOSLSKMKVQDPDPAANLYVAIPGS 227

Qy 362 KSFSEVELELEGDKVYHVSLSKVANSGV-SRSSINVFOSLSKMKVQDPDPAANLYVAIPGS 227

Db 363 YPRRLRASWTPASWPQCPHFLKFLQYRPAQHPTVPLQYRPAQHPA 267

Qy 363 YPRRLRASWTPASWPQCPHFLKFLQYRPAQHPTVPLQYRPAQHPA 267

Db 364 KSFSEVELELEGDKVYHVSLSKVANSGV-SRSSINVFOSLSKMKVQDPDPAANLYVAIPGS 227

Qy 364 KSFSEVELELEGDKVYHVSLSKVANSGV-SRSSINVFOSLSKMKVQDPDPAANLYVAIPGS 227

Db 365 KSFSEVELELEGDKVYHVSLSKVANSGV-SRSSINVFOSLSKMKVQDPDPAANLYVAIPGS 227

Qy 365 KSFSEVELELEGDKVYHVSLSKVANSGV-SRSSINVFOSLSKMKVQDPDPAANLYVAIPGS 227

Db 366 KSFSEVELELEGDKVYHVSLSKVANSGV-SRSSINVFOSLSKMKVQDPDPAANLYVAIPGS 227

Qy 366 KSFSEVELELEGDKVYHVSLSKVANSGV-SRSSINVFOSLSKMKVQDPDPAANLYVAIPGS 227

Db 367 L-VAGGSLSAFLGLLVCFLRLKKWKWSQAEEKESKTTSPPPYPLGPKPTFL--LVPLLT 423

Qy 367 L-VAGGSLSAFLGLLVCFLRLKKWKWSQAEEKESKTTSPPPYPLGPKPTFL--LVPLLT 423

Db 368 QGLHTQPEVERQDVSPAPRPSLQPHPRLLDHDH---SVEQAVAYA-SLGLLSF 377

Qy 368 QGLHTQPEVERQDVSPAPRPSLQPHPRLLDHDH---SVEQAVAYA-SLGLLSF 377

Db 369 PC---PQDFLGAACRVVIGGAEFSQYRNTEVNLPLGAS-TRLDVSYLQSLIRPDPPOG 223

Qy 369 PC---PQDFLGAACRVVIGGAEFSQYRNTEVNLPLGAS-TRLDVSYLQSLIRPDPPOG 223

Db 370 PQQYSEQSQRFSQCOLAVENTS-SFYIVSMCVYASSVGVSQCEWGPRTSPSTLTT 221

Qy 370 PQQYSEQSQRFSQCOLAVENTS-SFYIVSMCVYASSVGVSQCEWGPRTSPSTLTT 221

Db 371 DAAGLPHAVRVSARDFLDLAGTWSTWSPSWAGTSTGTLPKEIPTAWGQLHTQPEVEPOVD 341

Qy 371 DAAGLPHAVRVSARDFLDLAGTWSTWSPSWAGTSTGTLPKEIPTAWGQLHTQPEVEPOVD 341

Db 372 DAWSSLRHYVQLRQAEFFGGGEWSNEWSPEAMGTWTES-----RSPPAENEVS 328

Qy 372 DAWSSLRHYVQLRQAEFFGGGEWSNEWSPEAMGTWTES-----RSPPAENEVS 328

Db 373 SPAPERPSLQPHPRLLDHRSHRSQEVYAGA-----LASIGLISFLGFLYAGA----- 388

Qy 373 SPAPERPSLQPHPRLLDHRSHRSQEVYAGA-----LASIGLISFLGFLYAGA----- 388

Db 374 TPMQALTNTNDDDNIL-FRDSANATSLSLVPDSSVYPLPTFL-VAGGSLSAFLLICIAIVL 386

Qy 374 TPMQALTNTNDDDNIL-FRDSANATSLSLVPDSSVYPLPTFL-VAGGSLSAFLLICIAIVL 386

Db 375 -----LW-LRLRRGGKDGSKPKGFLASAVIPVDRRP 417

Qy 375 -----LW-LRLRRGGKDGSKPKGFLASAVIPVDRRP 417

Db 376 RFKKTKWKLRLAKEGRTSMHPPYSLGQLVPRPRP 420

Qy 376 RFKKTKWKLRLAKEGRTSMHPPYSLGQLVPRPRP 420

RESULT 10

150455 prolactin receptor - pigeon

C;Species: Columba livia (domestic pigeon)

C;Date: 13-Sep-1996 #sequence_revision 13-Sep-1996 #text_change 28-Jul-2000

C;Accession: I50455

R;Chen, X.; Horseman, N. D.

Endocrinology 135, 269-276, 1994

A;Title: Cloning, expression, and mutational analysis of the pigeon prolactin receptor

A;Reference number: I50455; MUID:34283267; PMID:516866

A;Status: preliminary; translated from GB/EMBL/DBBJ

A;Molecule type: mRNA

A;Residues: 1-830 <CHE>

A;Cross-references: EMBL:U07694; NID:9466381; PID:AAA20646.1; PMID:9466382

C;Superfamily: cytokine receptor homology <CRS1>

F;36-24/26/Domain: cytokine receptor homology <CRS2>

Query Match 9.7%; Score 221; DB 2; Length 830;

Best Local Similarity 29.0%; Pred. No. 4e-07; Indels 36; Mismatches 90; Gaps 38; Gaps 12;

C;Keywords: acute phase; cytokine receptor; transmembrane protein

F;1-19/Domain: signal sequence #status predicted <SIG>

Qy 111 YPPARPVVSCQAADYENFNSCTWSPSQISGLPTRYLSYRKTKVILGADSQRSPSTGPWPC 170

RESULT 9

A37986 interleukin-6 receptor precursor - rat

N;Alternate names: IL-6 receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999

R;Accession: A37986

R;Baumann, M.; Baumann, H.; Fey, G. H.

J. Biol. Chem. 265, 19853-19862, 1990

A;Title: Molecular cloning, characterization and functional expression of the rat liver

A;Reference number: A37986; MUID:91060602; PMID:2174054

A;Accession: A37986

A;Molecule type: mRNA

A;Residues: 1-462 <BAU>

A;Cross-references: GB:MS58587; PID:9204921; PID:g204922

C;Comment: After binding IL-6, this chain associates with a 130K glycoprotein that is expressed in the liver.

C;Superfamily: ciliary neurotrophic factor receptor homology; immunoglobulin

C;Keywords: acute phase; cytokine receptor; transmembrane protein

RESULT 9

A37986 interleukin-6 receptor precursor - rat

N;Alternate names: IL-6 receptor

C;Species: Rattus norvegicus (Norway rat)

C;Date: 30-Jun-1993 #sequence_revision 30-Jun-1993 #text_change 22-Jun-1999

R;Accession: A37986

R;Baumann, M.; Baumann, H.; Fey, G. H.

J. Biol. Chem. 265, 19853-19862, 1990

A;Title: Molecular cloning, characterization and functional expression of the rat liver

A;Reference number: A37986; MUID:91060602; PMID:2174054

A;Accession: A37986

A;Molecule type: mRNA

A;Residues: 1-462 <BAU>

A;Cross-references: GB:MS58587; PID:9204921; PID:g204922

C;Comment: After binding IL-6, this chain associates with a 130K glycoprotein that is expressed in the liver.

C;Superfamily: ciliary neurotrophic factor receptor homology; immunoglobulin

C;Keywords: acute phase; cytokine receptor; transmembrane protein

RESULT 11

Db 27 YPGKPKIIRCSLEKEETFSCWKPSGDSLGLPTNTLFYSK----DSEERKI----YEC 75
 A;Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin receptor gene variants in cattle
 A;Reference number: I45971; PMID:33246019; MUID:1338725
 A;Accession: I45971
 A;Species: Bos primigenius taurus (cattle)
 A;Molecule type: mRNA
 A;Residues: 1-581 <SCo>
 A;Cross-references: GB:L02549; PID:9163617; PIDN:AAA51417.1; PID:9163618
 C;Genetics:
 A;Gene: PRLR
 C;Superfamily: cytokine receptor homology
 F;36-221/Domain: cytokine receptor homology <CRS>

Query Match 9.0%; Score 204.5; DB 2; Length 581;
 Best Local Similarity 26.5%; Pred. No. 3.4e-06;
 Matches 61; Conservative 36; Mismatches 92; Indels 41; Gaps 11;

Qy 171 PQDPL-GAARGCV--HGAEEFWQSYRINVTENVNPLGAST--RLLDVSLQSILRDPDPQGL 224
 C;Species: Gallus gallus (chicken)
 C;Date: 30-Sep-1993 # sequence_revision 30-Sep-1993 #text_change 28-Jul-2000
 C;Accession: JQ1655
 R;Tanaka, M.; Maeda, K.; Okubo, T.; Nakashima, K.
 Biochem. Biophys. Res. Commun. 188, 490-496, 1992
 A;Title: Double antenna structure of chicken prolactin receptor deduced from the cDNA sequence
 A;Reference number: JQ1655; MUID:93075121; PMID:1445292
 A;Molecule type: mRNA
 A;Residues: 1-831 <TA>
 A;Cross-references: DDBJ:D13154; NID:9222848; PIDN:BAA02439.1; PID:9222849
 A;Experimental source: kidney
 C;Superfamily: cytokine receptor homology
 C;Keywords: glycoprotein; transmembrane protein
 F;1-23/Domain: signal sequence #status predicted <SIG>
 F;36-219/Domain: prolactin receptor #status predicted <MAT>
 F;29-425/Domain: cytokine receptor homology <CRS2>
 F;439-91,100,112,132,262,303,315,335,647,701,800/Binding site: carbohydrate (Asn) (covalent)

Query Match 9.4%; Score 214; DB 2; Length 831;
 Best Local Similarity 27.5%; Pred. No. 1.2e-06;
 Matches 76; Conservative 42; Mismatches 108; Indels 50; Gaps 15;

Qy 113 PAP-VVSCQADYENFSCWPSQISGLPTRYLTSRKTKTVLGADSQRSSSTGPWPPCP 171
 Db 28 PRGPKIIIRCSLEKEETFSCWKPSGDSLGLPTNTLFYSK----DSEEEI----YECP 76
 A;Title: Molecular cloning of the bovine prolactin receptor and distribution of prolactin receptor gene variants in cattle
 A;Reference number: I45971; PMID:33246019; MUID:1338725
 A;Accession: I45971
 A;Species: Bos primigenius taurus (cattle)
 A;Molecule type: mRNA
 A;Residues: 1-581 <SCo>
 A;Cross-references: GB:J04510; PID:9165669; PIDN:AAA31457.1; PID:9165670
 R;Waters, M.J.; Spencer, S.A.; Hamlin, G.; Henzel, W.J.; Wood, W.I.
 Int. J. Biochem. 22, 1089-1095, 1990
 A;Title: Purification and partial sequence of the rabbit mammary gland prolactin receptor
 A;Reference number: A30304; MUID:89184578; PMID:228321
 A;Accession: A30304
 A;Molecule type: mRNA
 A;Residues: 1-616 <EDEN>
 A;Cross references: R;Alderson, R.; Spencer, S.A.; Hamlin, G.; Henzel, W.I.; Wood, W.I.
 Int. J. Biochem. 22, 1089-1095, 1990
 A;Title: Purification and partial sequence of the rabbit mammary gland prolactin receptor
 A;Reference number: A60380; MUID:91146782; PMID:2289615
 A;Accession: A60380
 A;Molecule type: protein
 A;Residues: 1-58
 A;Note: the amino acid sequence of the mature protein was blocked
 C;Superfamily: cytokine receptor homology
 C;Keywords: blocked amino end; glycoprotein; transmembrane protein
 F;1-24/Domain: signal sequence #status predicted <SIG>
 F;25-616/Product: prolactin receptor 2 #status predicted <MAT>
 F;235-258/Domain: cytokine receptor homology <CRS>
 F;59,104,132,347,389,411/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 9.0%; Score 204; DB 2; Length 616;
 Best Local Similarity 27.7%; Pred. No. 3.9e-06;
 Matches 66; Conservative 29; Mismatches 95; Indels 48; Gaps 13;

Qy 112 PPAP-VVSCQADYENFSCWPSQISGLPTRYLTSRKTKTVLGADSQRSSSTGPWPPC 170
 C;Species: Bos primigenius taurus (cattle)
 C;Date: 16-Aug-1996 # sequence_revision 16-Aug-1996 #text_change 28-Jul-2000
 C;Accession: I45971
 R;Scott, P.; Kessler, M.A.; Schuler, L.A.
 Mol. Cell. Endocrinol. 89, 47-58, 1992

Db 27 PGKPSIFKCRSPKEETFCWRPGADGGLPTNTLYHKE----GETTHEC 75

Qy 171 PQDPLGAAARCVHGG--AEFWSQYRINVTEVNPLGAST--RLDVSLSQSLRDPDPQGL 224

Dbb	76	PDYKTPGGPNSCYFSKKHHSIWTTIVTITVATNOMGSSVSDERYDVTY--IVEPDPPBVNL	133
Qy	225	RVESVPGVPRR - LRASTWTP -- -ASWPQCPHPLKLFRQLYRAQHPWAWSVEAGL	276
Dbb	134	TLEKXHPDERKPWLWKVWLPPTLYDVRSGW ---LTLQBIRLKPEKAQWET-HFAGQ	187
Qy	277	EE - VITDAVAGLPHAVRYSARDELDAQTNSTWSPEAWGTGSTGTP-----KEIPAW	327
Dbb	188	OTOKFILSLYPGOXYLVORCKP -- DHGFNSWVSSW -----SSTOPIIDETMKMWTW	238

RESULT 14
BSA405
prostaglandin receptor short form slb precursor, breast cancer cells T-47D - human

C. Accession number: B59405; PMID: B4400
R.; Hu, Z.; Meng, J.; Dufour, M.L.
J.; Biol. Chem. 276, 41086-41094, 2001
A. Title: Isolation and characterization of two novel forms of the human prolactin
Reference number: A59405; PMID: 11518703
MNTD:21538812; PMID:11518703

A; Reference number: A49400
A; Accession: B49400

A. Residues: 1-288 <H02>
A. Cross references: GB:AF214012; PIDN:AF214012.1
A. Comments: This is one of the short forms (AF214012.1 and AF214012) of the human protein.

C;genetics: GDB:PRLR
A,A, Gene: GDB:120315; OMIM:17761
A,A, Cross references: GDB:120315;
A,A, Map position: 5p13.3-5p13.1

<SIG> EF_1-24 /Domain: signal sequence #status predicted <MAT>
<LIG> EF_25-288 /Domain: prolactin receptor, short form Sib #status predicted <MAT>

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Query Match Post Locality Similarity Score 189; DB 2; Length 288;
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112 PPARP-VVSQAAODYENFSCTWSPSQISGLPTRYLTSYRKKTIVLGADSQRSPSTGPWPC 170
QY

171 PODPLGAARCCVHGAEF -- WSOYRINTVEVNPIGAS -TRILPDYSSOSILRPDPEOGRLRV 226

EL	/S	FULLYOCHEURQVIIJUNWKLIMMVNPINQMGTSFSDUELLVUVIIVQDFDULAV	133
EL	/S	ESVPGYPRR - L-RASWNTYP-----ASWPQCPHFLIKFRFLQRPAQHPAWSVEPAG--L	276
QY	227	ESVPGYPRR - L-RASWNTYP-----ASWPQCPHFLIKFRFLQRPAQHPAWSVEPAG--L	276

277 EEVITDAVAGLPHAVRVSARDFELDAGTWSTWSP 309
QY

RESULT 15 AS4405 prolactin receptor short form S1a precursor, breast cancer cells T-47D - human

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:38:14 ; Search time 13 Seconds
(without alignments)
645.0287 Million cell updates/sec

Title: US-09-924-338-2
Perfect score: 2275
Sequence: 1 MSSSSGGLSRVLYAVATALV KFGFLASVIPYDRPGAPNL 422

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 120991 seqs, 19878514 residues

Total number of hits satisfying chosen parameters: 120991

Minimum DB seq length: 0
Maximum DB seq length: 20000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published_Applications_AA:*

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2: /cgn2_6/podata/1/pubpaas/US09_NEW_PUB.pep:*

3: /cgn2_6/podata/1/pubpaas/US06_NEW_PUB.pep:*

4: /cgn2_6/podata/1/pubpaas/US06_PUBCOMB.pep:*

5: /cgn2_6/podata/1/pubpaas/US07_NEW_PUB.pep:*

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14: /cgn2_6/podata/1/pubpaas/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2275	100.0	422	10 US-09-924-338-2	Sequence 2, Appli
2	1831	80.5	441	10 US-09-924-338-4	Sequence 4, Appli
3	339	14.9	1158	9 US-09-935-866-26	Sequence 26, Appli
4	332	14.6	1168	9 US-09-935-866-24	Sequence 24, Appli
5	329.5	14.5	360	5 9 US-09-935-866-15	Sequence 15, Appli
6	329.5	14.5	592	9 US-09-935-866-8	Sequence 8, Appli
7	313	13.8	315	9 US-09-935-866-16	Sequence 16, Appli
8	255.5	11.2	229	9 US-10-000-776-10	Sequence 10, Appli
9	255.5	11.2	229	9 US-09-911-497-12	Sequence 12, Appli
10	212.5	9.3	389	10 US-09-880-578-27	Sequence 27, Appli
11	211.5	9.3	389	10 US-09-880-578-24	Sequence 24, Appli
12	211.5	9.3	389	10 US-09-880-578-29	Sequence 29, Appli
13	211.5	9.3	421	9 US-09-037-657-44	Sequence 44, Appli
14	211.5	9.3	422	9 US-09-94-413-32	Sequence 32, Appli
15	211.5	9.3	422	9 US-09-94-403-32	Sequence 32, Appli
16	211.5	9.3	422	9 US-09-94-896-32	Sequence 32, Appli
17	211.5	9.3	422	9 US-09-94-944-32	Sequence 32, Appli
18	211.5	9.3	422	9 US-09-94-907-32	Sequence 32, Appli
19	211.5	9.3	422	9 US-09-94-929-32	Sequence 32, Appli

ALIGMENTS

RESULT 1
US-09-924-338-2

; Sequence 2, Application US/09924338
; Patent No. US200200233A1

; GENERAL INFORMATION:

; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLUEKIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA

; ZIP: 02140

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/924,338
FILING DATE: 07-Aug-2001
CLASSIFICATION: <Unknown>
PRIORITY APPLICATION NUMBER: 09/151,102
APPLICATION NUMBER: 09/151,102
FILING DATE: 1998-09-00
APPLICATION NUMBER: 08/362,304
FILING DATE: 22-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: GT5252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 422 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Query Match 100.0%; Score 2275; DB 10; Length 422;

Best Local Similarity 100.0%; Pred. No. 5e-144;
Matches 422; Conservative 0; Mismatches 0; Gaps 0;

Qy 1 MSSSSGLSRVIVAVATLYSASSCPQAMPGPPGQYQGPGRSVYLCCPGVTAGDPVSWF 60

Db 1 MSSSSGLSRVIVAVATLYSASSCPQAMPGPPGQYQGPGRSVYLCCPGVTAGDPVSWF 60

Qy 61 RDGEPKLQLQGPDGLIGHELVLAQADSTDCTSYKICQTLQALGTTVLQGYPPARPVSC 120

Db 61 RDGEPKLQLQGPDGLIGHELVLAQADSTDCTSYKICQTLQALGTTVLQGYPPARPVSC 120

Qy 121 QAADYENFNSCTWSPSQTSQPLTRVLTYSRKTKTIVLAGDSORRSPSTGTLQALGTTVLQGYPPARPVSC 180

Db 121 QAADYENFNSCTWSPSQISGLPLTRVLTYSRKTKTIVLAGDSORRSPSTGTLQALGTTVLQGYPPARPVSC 180

Qy 181 VVHGAEEFWSOYRINTEVNPLGASTRLDVSLSQSLRRDPQGJURVEVSPGYPRRLRASW 240

Db 181 VVHGAEEFWSOYRINTEVNPLGASTRLDVSLSQSLRRDPQGJURVEVSPGYPRRLRASW 240

Qy 241 TYPASWPCOPHFLIKERLOYRPAOHAWNSTVEPAGLEEVITDAVAGLPHAVRYSARDFLD 300

Db 241 TYPASWPCOPHFLIKERLOYRPAOHAWNSTVEPAGLEEVITDAVAGLPHAVRYSARDFLD 300

Qy 301 AGTWSTWSPEAWGTPSTGTIPKEIPAWGQLHTQPEVEQVDSRAPPRLQHPRLDHR 360

Db 301 AGTWSTWSPEAWGTPSTGTIPKEIPAWGQLHTQPEVEQVDSRAPPRLQHPRLDHR 360

Qy 361 DSVEQVAVLASLGLTISFLGLVAGALGIWLRURGGDKGSKPGEFLASVIVPDRRGPSA 420

Db 361 DSVEQVAVLASLGLTISFLGLVAGALGIWLRURGGDKGSKPGEFLASVIVPDRRGPSA 420

Qy 421 NL 422

Db 421 NL 422

RESULT 2

US-09-924-338-4

; Sequence 4, Application US/09924338

; Patent No. US20020083233A1

; GENERAL INFORMATION:

; APPLICANT: Tobin, James

; TITLE OF INVENTION: HUMAN INTERLEUKIN-11 RECEPTOR

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 Cambridgepark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/924,338

; FILING DATE: 07-Aug-2001

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 09/151,102

; FILING DATE: 1998-09-10

; APPLICATION NUMBER: 08/362,304

; FILING DATE: 22-DEC-1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Brown, Scott A.

; REGISTRATION NUMBER: 32,724

; REFERENCE/DOCKET NUMBER: G15252

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (617) 498-8224

; TELEFAX: (617) 876-5851

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 441 amino acids

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

; US-09-924,338-4

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2; Gaps 1;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

; SEQ ID NO: 4:

; Query Match 80.5%; Score 1831; DB 10; Length 441;

; Best Local Similarity 83.1%; Pred. No. 1.5e-14; Mismatches 50; Indels 2;

; Matches 340; Conservative 17; Mismatches 17; Indels 2;

RESULT 4
US-09-935-868-24
; Sequence 24, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc.
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQ ID NO: 15
; LENGTH: 360;
; Query Match Score 329.5; DB 9; Length 360;
; Best Local Similarity 29.2%; Pred. No. 4; 8e-15;
; Matches 112; Conservative 46; Mismatches 172; Indels 53; Gaps 15;

Qy 63 GEPKLLQGP-----SGIGHELYLAQADSTDEGTYICOTLDGALGGTVTLQGYPPA 114
Db 61 ----VLRKPAAGSHPSRWAQGRRLILLRSVQHDSNNSCYRA-GRPAQTVHLVVDPPE 115

Qy 115 RPVVSQ-QAADDENFSCTWPSQISLPLRTYLTSLRQHPSKTKTIGADSQRSSSTG-PWPC-- 170
Db 116 EPQLSCFRKSPLSNVYCEWGRPSTSLLT-----KAVLLVRKFQNSAEDFQEPQCQY 167

Qy 171 -PQDPLGAARCVHQAEEFSQYRQINTEVNPGLAS-TRILDVSLQSILRPDPPOGLRVE 227

Db 168 SQESQFSCOLAVPEEDS--SFYIVSMCVAASSVGSKFSKQTFOQCGILQDPDPPANITVPT 225

Qy 228 SVPGYPRRLRASWTPASWPCQPHFLKFLRQYRPAQHPAWSTVEPAGEE--VITDAVA 285
Db 226 AVARNPRLWSTWQDHSHWN-SSFYFLRFLRYRAERSKTTTWAKVDLQHCVTHDANS 284

Qy 286 GLPHAVRVSARDFLDAGTWSWSPAWGTPSTGTIPKEIPIAWGQHTQPEVQDPSAP 345
Db 285 GLRHVYQLRAQEFGQGEWSEWSPEAMGTWTES--RSPPAENEVSTPMELUDPGCYISP 342

Qy 346 PRPSLQPH 353
Db 343 ESPVWQLH 350

RESULT 5
US-09-935-868-15
; Sequence 15, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc.
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 15
; LENGTH: 360
; TYPE: PRT
; ORGANISM: Homo sapiens
; SEQ ID NO: 15
; LENGTH: 360;
; Query Match Score 329.5; DB 9; Length 360;
; Best Local Similarity 29.2%; Pred. No. 4; 8e-15;
; Matches 112; Conservative 46; Mismatches 172; Indels 53; Gaps 15;

Qy 5 CGSLSRVLYVATALYSASSPCPOAWGPPGQYQGGRSYKLCCPQGVTAQD--PVSFERD 62
Db 6 CALLAALLAAFGAAL--APRRCPAQAVARGVLTSLQGDSVTLCPCVEPEDNATVHW--- 60

Qy 63 GEPKLLQGP-----SGIGHELYLAQADSTDEGTYICOTLDGALGGTVTLQGYPPA 114
Db 61 ----VLRKPAAGSHPSRWAQGRRLILLRSVQHDSNNSCYRA-GRPAQTVHLVVDPPE 115

Qy 115 RPVVSQ-QAADDENFSCTWSSSQISGLPTRYLTSKFKTVLJADSRRRSPTG - PWPC-- 170
Db 116 EPQLSCFRKSPLSNVYCEWGRPSTSLLT-----KAVLLVRKFQNSPAEDFQPCQY 167

Qy 171 -PQDPLGAARCVHQAEEFSQYRQINTEVNPGLAS-TRILDVSLQSILRPDPQQLRVE 227
Db 168 SQESQFSCOLAVPEEDS--SFYIVSMCVAASSVGSKFSKQTFOQCGILQDPDPPANITVPT 225

Qy 228 SVPGYPRRLRASWTPASWPCQPHFLKFLRQYRPAQHPAWSTVEPAGEE--VITDAVA 285
Db 226 AVARNPRLWSTWQDHSHWN-SSFYFLRFLRYRAERSKTTTWAKVDLQHCVTHDANS 284

Qy 286 GLPHAVRVSARDFLDAGTWSWSPAWGTPSTGTIPKEIPIAWGQHTQPEVQDPSAP 345
Db 285 GLRHVYQLRAQEFGQGEWSEWSPEAMGTWTES--RSPPAENEVSTPMQ 332

Qy 346 PRPSLQPHPRLLDHRDSVEQAV 368
Db 333 ALTTNKDDDNIL-FRDSANATSL 354

RESULT 6
US-09-935-868-8
; Sequence 8, Application US/09935868
; Patent No. US20020164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc.
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935,868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 8

LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-8

Query Match 14.5%; Score 329.5; DB 9; Length 592;
Best Local Similarity 29.2%; Pred. No. 8 4e-15;
Matches 112; Conservative 46; Mismatches 172; Indels 53; Gaps 15;

QY 5 CSGLSRVLVAVATALVASSSPCPOAWGPGVQYQGPERSVKLCCPGVTTAGD--PVSMFRD 62
Db 6 CALLAALAAAPGAAL- APRCPAQEVARGVLTSLPGDSVTLCPGVEPEDNATVHW-- 60

QY 63 GEPKLLQGPD-----SGLGHLVLAQADSDTEGTYICQTLGALGGTVTQLGYPPA 114
Db 61 ----VLRKPAAGSHPSRVMAGMGRLLRSVOLHDSGNNSCYRA-GPAGTVHLDVPP 115

QY 115 RPVYSC-QAAYDENFSCTWSPSQTSGLPLTRYLTSYRKTVLGADSQRSSPSTG-PWPC-- 170
Db 116 EPOLSCFRKSPLSNVCEMGRSTPLTT-----KAVLVLVRKFQNSPAEDFQEPCQY 167

QY 171 -PQDPGLARCVHGA-EFWSPQRINTVEVNPGAS-TRLIIVSLSQSLRPPPOGLRVE 227
Db 168 SQESQFKSFCOLQAVEPEGDS--SFIVTIVSMCVASSYGSKEFKTQTFQCGCILQQPDPANITVT 225

QY 228 SVPGYPRRLRASWTYPAWPCQPHFLKFRQLYRPQAHPAWSITIVEPAGLEE--VITDVA 285
Db 226 AVARNPRNLISVNTQDPSKHN-SSFYRLRFELRTRAERSKTFITWMVRLDQHHCVIHDWS 284

QY 286 GLPHAVRVSARDFLDAGTWSTWSPEAWGTPSTGTIPKEIPANCQQLTOPEBEFQVDSPAP 345
Db 285 GLRHVVQLRAQUEFGQEMSEWSPEAMGTPWTE-----RSPPAENEVSTPMQ 332

QY 346 PRPSLQPHPRLDSDYEQVAV 368
Db 333 ALTNKDDDNL-FRDSANATL 354

RESULT 7
US-09-935-868-16
; Sequence 16, Application US/09935868
; Patent. No. US2002-0164690A1
; GENERAL INFORMATION:
; APPLICANT: Regeneron Pharmaceuticals, Inc
; TITLE OF INVENTION: Receptor Based Antagonists, and Methods of Making and Using
; FILE REFERENCE: REG 203D
; CURRENT APPLICATION NUMBER: US/09/935, 868
; CURRENT FILING DATE: 2002-04-11
; PRIOR APPLICATION NUMBER: PCT/US99/22045
; PRIOR FILING DATE: 1999-09-22
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 16
; LENGTH: 315
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-935-868-16

Query Match 13.8%; Score 315; DB 9; Length 315;
Best Local Similarity 31.0%; Pred. No. 3.8e-14;
Matches 102; Conservative 38; Mismatches 149; Indels 40; Gaps 13;

QY 5 CSGLSRVLVAVATALVASSSPCPOAWGPGVQYQGPERSVKLCCPGVTTAGD--PVSMFRD 62
Db 6 CALLAALAAAPGAAL- APRCPAQEVARGVLTSLPGDSVTLCPGVEPEDNATVHW-- 60

QY 63 GEPKLLQGPD-----SGLGHLVLAQADSDTEGTYICQTLGALGGTVTQLGYPPA 114
Db 61 ----VLRKPAAGSHPSRVMAGMGRLLRSVOLHDSGNNSCYRA-GPAGTVHLDVPP 115

QY 115 RPVYSC-QAAYDENFSCTWSPSQTSGLPLTRYLTSYRKTVLGADSQRSSPSTG-PWPC-- 170
Db 116 EPOLSCFRKSPLSNVCEMGRSTPLTT-----KAVLVLVRKFQNSPAEDFQEPCQY 167

QY 171 -PQDPGLARCVHGA-EFWSPQRINTVEVNPGAS-TRLIIVSLSQSLRPPPOGLRVE 227
Db 168 SQESQFKSFCOLQAVEPEGDS--SFIVTIVSMCVASSYGSKEFKTQTFQCGCILQQPDPANITVT 225

QY 228 SVPGYPRRLRASWTYPAWPCQPHFLKFRQLYRPQAHPAWSITIVEPAGLEE--VITDVA 285
Db 226 AVARNPRNLISVNTQDPSKHN-SSFYRLRFELRTRAERSKTFITWMVRLDQHHCVIHDWS 284

QY 286 GLPHAVRVSARDFLDAGTWSTWSPEAWGTPSTGTIPKEIPANCQQLTOPEBEFQVDSPAP 345
Db 285 GLRHVVQLRAQUEFGQEMSEWSPEAMGTPWTE-----RSPPAENEVSTPMQ 332

QY 346 PRPSLQPHPRLDSDYEQVAV 368
Db 333 ALTNKDDDNL-FRDSANATL 354

RESULT 8
US-10-000-776-10
; Sequence 10, Application US/10000776
; Patent. No. US20020164609A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.
; APPLICANT: Pfanz, Stefan K.-H.
; APPLICANT: Kastlein, Robert A.
; APPLICANT: Basan, Jose P.
; APPLICANT: Renick, Donna
; APPLICANT: de Waal Maleyt, Rene
; APPLICANT: Cheung, Jeanne
; TITLE OF INVENTION: MAMMALIAN CYTOKINES; RELATED REAGENTS
; FILE REFERENCE: DX01040K3
; CURRENT APPLICATION NUMBER: US/10/000,776
; CURRENT FILING DATE: 2001-11-30
; PRIOR APPLICATION NUMBER: 09/791,497
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 09/627,887
; PRIOR FILING DATE: 2000-07-27
; PRIOR APPLICATION NUMBER: 60/146,581
; PRIOR FILING DATE: 1999-07-30
; PRIOR APPLICATION NUMBER: 60/147,763
; PRIOR FILING DATE: 1999-08-06
; NUMBER OF SEQ ID NOS: 13
; SEQ ID NO: 10
; LENGTH: 229
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-776-10

Query Match 11.2%; Score 255.5; DB 9; Length 229;
Best Local Similarity 30.9%; Pred. No. 2.4e-10;
Matches 73; Conservative 35; Mismatches 95; Indels 33; Gaps 10;

QY 94 CQTLDGAGLGTVTLGQPPAR--PVVSCQAADYE-NFSCWMS--PQIQSGLPTRVLYTS 147
Db 15 CPCCGRGK-----PPAALTLPQCRCRSPVIAVDCSKTLPPAPNSTSPVSFAT 65

QY 148 YRKRTVLGADSQRSPSTGWPQPCQDPPLGAARCVRGAEEFSQ--YRINVTEVNPLGAST 205
Db 66 YR---LGMARGHS---WPLQQTPTSTSCITDQFLSMSAPVILVNTAVHPGSS 116

QY 206 RLIDVLSILIRPDPPQSLRVESVPGYPRRLRASWTVASWPCQPHFLKFRQLYRPQHQ 265
Db 117 SFVPFITEIIKPDPPGEVRLS - PLARHRVQVQWEPPGSMWPEFEISKYWRYKROGA 174

QY 266 PMSTVEPAGLEEVITDAGTWSWSPAWGTPSTG 318
Db 175 ARFHVGPIEATSFILRRAVR--PRARYVQVAQDLTUYGELSDWSLFATATMSLG 228

RESULT 9
US-09-791-497-12
; Sequence 12, Application US/09/791497
; Publication No. US20030000343A1
; GENERAL INFORMATION:
; APPLICANT: Timans, Jacqueline C.

APPLICANT: Kastelein, Robert A.
 APPLICANT: Bazan, J. Fernando
 APPLICANT: Pflanz, Stefan
 TITLE OF INVENTION: Mammalian Cytokines; Related Reagents
 FILE REFERENCE: DX0104OK2
 CURRENT APPLICATION NUMBER: US/09/791,497
 CURRENT FILING DATE: 2001-02-22
 PRIOR APPLICATION NUMBER: 60/146,581
 PRIOR FILING DATE: 1999-07-30
 PRIOR APPLICATION NUMBER: 60/147,763
 PRIOR FILING DATE: 1999-08-06
 NUMBER OF SEQ ID NOS: 14
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO: 12
 LENGTH: 229
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-791-497-12

Query Match 11.28; Score 255.5; DB 9; Length 229;
 Best Local Similarity 30.98; Pred. No. 2.4e-10;
 Matches 73; Conservative 35; Mismatches 95; Indels 33; Gaps 10;

Qy 94 COTLDGALGGIVTLQGYPPAR--PVSICAOADYE-NFSCTWS--PSQISGLPTRYLT S 147
 Db 15 CPPCSGRKG -----PAAATLTERVQCRASRYPIAVDCSWTLPAPNSTSPSFIAH 65

Qy 148 YRKKTIVLGADSQRSPSTGPWPCPDPGLAARCVYHGAEFWSQ--YRINTYEVNPLGAST 205
 Db 66 YR---LGMARGHS---WFCLOQTPTSCTIDVQLSMAPVLYNTAVHPWGSS 116

Qy 206 RLLDVSQSLIRPDPDPOGLRASVTPYPAWSICOPHFLKFLRQLYRPQAH 265
 Db 117 SFVPFITEHKPDPPGVRLS--PLAERHQVQNEPPGSMWPPEIFSLXWIRYKROGA 174

Qy 266 PAWSVTEPAGELEEVITDAVAGLPH -- VRVSAARDLDAQMWSTSWPEANQTPSTG 318
 Db 175 ARFHRYGPIEATSFLRAVR--PRARYYYQVAQDLTDYGEISDNLSNLPATMSLG 228

RESULT 10
 US-09-880-578-27
 ; sequence 27, Application US/09880578
 ; Patent No. US2002004573A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lok, Si
 ; APPLICANT: Presnell, Scott R.
 ; APPLICANT: Gilbert, Anna C.
 ; Foster, Donald C.
 ; Adams, Robyn L.

TITLE OF INVENTION: MAMMALIAN ZCYTORS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics
 STREET: 1201 Eastlake Ave East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/880,578
 FILING DATE: 13-Jun-2001
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:

APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G.
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: 96-22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 27:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 39 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 27:
 US-09-880-578-27

Query Match 9.38; Score 212.5; DB 10; Length 389;
 Best Local Similarity 23.88; Pred. No. 3e-07;
 Matches 89; Conservative 54; Mismatches 136; Indels 95; Gaps 19;

Qy 17 TALVASSSSPCPAWGPVGQVQGPGRSVKLCC----PGVTAGDPPVSWFRIDGE---PKL 67
 Db 3 TAVISQDPTILLI-----GSULLACATSVHSDPPGATA-EISYWTINLRLLPPE 50

Qy 68 LOGPDSGLIGHELVLAQD----STDGEETYCQTLDALGGFTVOLGYPPARPV-VSCQ 121
 Db 51 SRVLNAs--TIALALANLNGSRQRSSDNLYCHARDSTILAGSCLVGLPPPKPVNISCW 107

Qy 122 AADYENFSCTNSPSQ--TSGLPTRTRYLTSYRKTVLGADSQRSRSPTGPWPC -PODPLGA 177
 Db 108 SKRNKDJTCRWPGAIGETFLHTNYSILKURWGGDNTCEYHTGPHSCHIKD---- 163

Qy 178 ARCVVHGAEEFNSQYRINTEVNPGLAS-TRLVDLSLOSSILRDPDPPGLRVESYPGYPRRL 236
 Db 164 -----LALFPYEWATEANRGLGSSRSVDVLTLDLVVTTDPPPYHVSRYGGLEDQL 216

Qy 237 RASWTPASWPCQPHFL--KFLQKRPQHDWSVTP-------AGLBEVTDIAVA 285
 Db 217 SVRVWSP----PALKDFLQKAYQIIRQVEDSDWKVYDDVSNQTSCLAGLK-----P 266

Qy 286 GLPHAYVRSARDF---LDAGTWSTWS-PEA-----WGTPTSGTI 320
 Db 267 GIVYFWVRCNFGIYGSKRAGIWSMWSHPTAASTPRSERPGGGACEPRGEPPSGPV 326

Qy 321 PKEIP--ANGOLH 331
 Db 327 RRELKQFGLWKKH 340

RESULT 11
 US-09-880-578-24
 ; Sequence 24, Application US/09880578
 ; Patent No. US2002004573A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Lok, Si
 ; Presnell, Scott R.
 ; Gilbert, Anna C.
 ; Foster, Donald C.
 ; Adams, Robyn L.

TITLE OF INVENTION: MAMMALIAN ZCYTORS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics
 STREET: 1201 Eastlake Ave East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102

TITLE OF INVENTION: MAMMALIAN ZCYTORS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics
 STREET: 1201 Eastlake Ave East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA

ZIP: 98102
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/880,578
 FILING DATE: 13-Jun-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G.
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: 96-22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 TELEX: <Unknown>
 INFORMATION FOR SEQ ID NO: 24:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 389 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 24:
 US-09-880-578-24

Query Match 9.3%; Score 211.5; DB 10; Length 389;
 Best Local Similarity 23.8%; Pred. No. 3.5e-07; Indels 95; Gaps 19;
 Matches 89; Conservative 53; Mismatches 137; Delins 95; Gaps 19;

QY 17 TALVASSSPCPQANGPPGVQYQGPGRSYVKLC-----PGVTAGDPVSWFRDGE---PKL 67
 Db 3 TAVISPQDPTLLI-----GSSLLATCSVHGDPGATA-EGLYWTLNGRLPPEL 50

QY 68 LOGDGSGLGHELVIAQAD----STDEGTCTLDGAQGTVLQLQYPPRPV-VSCQ 121
 Db 51 SRLVNLAS--TIALALANINGSRQSGDNLVCHARDGSTLAGSCLYVGQPLPPXPNISCW 307

QY 122 AADYENFSCTWSPSQ--TSLGLPTRYLTSYRKTKYLGADSQRSPSTGPWPC--PQDPLGA 177
 Db 108 SKNMKDLICRWTPOSHGENFLHNYNSLYKLRAYQDNTCEHTVGHPSCHIPKD---- 163

QY 178 ARCVYHGAFFWSQYRINTVEVNPLG-ASTRLDVLSOSILRDPPOQGLRVESYPGYPRRL 236
 Db 164 -----LALETPYEIWTEATNRIGSANSDSLTDILDYVTTDPPPDVHVSRYVGGLEDQ 216

QY 237 RASVTPASWPCCOPHFL--KFRLQYRPAQHPAWSTVP-----AGLEEVITDAV 285
 Db 217 SVRNVSP--PAALKDFLQAKYQIRYRVEDSVDWKVDDNOTSCRLAGLK-----P 266

QY 286 GLPHAVRYSARDF----LDASTGWSTWSN-PEA-----WGTTPSTGTI 320
 Db 267 GTYVFVQRCNPPIGYGSKRAGIWSENSHPTAASTPRSERPSPGGGACEPRGEPPSGCPV 326

QY 321 PKEIP--AWGQLH 331
 Db 327 RRELKQFLGWLKHH 340

RESULT 12
 US-09-880-578-29
 Sequence 29, Application US/09880578
 Patent No. US20020045733A1
 GENERAL INFORMATION:
 APPLICANT: Loh, Si
 Presnell, Scott R.
 Jelberg, Anna C.
 Gilbert, Teresa

Foster, Donald C.
 Adams, Robyn L.
 Lehrer, Joyce M.
 TITLE OF INVENTION: MAMMALIAN ZCYTORS
 NUMBER OF SEQUENCES: 37
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: ZymoGenetics
 STREET: 1201 Eastlake Ave East
 CITY: Seattle
 STATE: WA
 COUNTRY: USA
 ZIP: 98102
 COMPUTER READABLE FORM:
 COMPUTER: IBM Compatible
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSeq for Windows Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/880,578
 FILING DATE: 13-Jun-2001
 CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: <Unknown>
 FILING DATE: <Unknown>
 ATTORNEY/AGENT INFORMATION:
 NAME: Lunn, Paul G.
 REGISTRATION NUMBER: 32,743
 REFERENCE/DOCKET NUMBER: 96-22
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 206-442-6627
 TELEFAX: 206-442-6678
 TELE: <Unknown>
 INFORMATION FOR SEQ ID NO: 29:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 389 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: Linear
 MOLECULE TYPE: protein
 SEQUENCE DESCRIPTION: SEQ ID NO: 29:
 US-09-880-578-29

Query Match 9.3%; Score 211.5; DB 10; Length 389;
 Best Local Similarity 24.1%; Pred. No. 3.5e-07; Mismatches 52; Delins 95; Gaps 19;

QY 17 TALVASSSPCPQAWGPPGVQYQGPGRSYVKLC-----PGVTAGDPVSWFRDGE--PKL 67
 Db 3 TAVISPQDPTLLI-----GSSLLATCSVHGDPGATA-EGLYWTLNGRLPPEL 50

QY 68 LOGDGSGLGHELVIAQAD----STDEGTCTLDGAQGTVLQLQYPPRPV-VSCQ 121
 Db 51 SRLVNLAS--TIALALANINGSRQSGDNLVCHARDGSTLAGSCLYVGQPLPPXPNISCW 307

QY 122 AADYENFSCTWSPSQ--TSLGLPTRYLTSYRKTKYLGADSQRSPSTGPWPC--PQDPLGA 177
 Db 108 SKNMKDLICRWTPOSHGENFLHNYNSLYKLRAYQDNTCEHTVGHPSCHIPKD---- 163

QY 178 ARCVYHGAFFWSQYRINTVEVNPLG-ASTRLDVLSOSILRDPPOQGLRVESYPGYPRRL 236
 Db 164 -----LALETPYEIWTEATNRIGSANSDSLTDILDYVTTDPPPDVHVSRYVGGLEDQ 216

QY 237 RASVTPASWPCCOPHFL--KFRLQYRPAQHPAWSTVP-----AGLEEVITDAV 285
 Db 217 SVRNVSP--PAALKDFLQAKYQIRYRVEDSVDWKVDDNOTSCRLAGLK-----P 266

QY 286 GLPHAVRYSARDF----LDASTGWSTWSN-PEA-----WGTTPSTGTI 320
 Db 267 GTYVFVQRCNPPIGYGSKRAGIWSENSHPTAASTPRSERPSPGGGACEPRGEPPSGCPV 326

QY 321 PKEIP--AWGQLH 331
 Db 327 RRELKQFLGWLKHH 340

RESULT 12
 US-09-880-578-29
 Sequence 29, Application US/09880578
 Patent No. US20020045733A1
 GENERAL INFORMATION:
 APPLICANT: Loh, Si
 Presnell, Scott R.
 Jelberg, Anna C.
 Gilbert, Teresa

QY 286 GLPHAVRYSARDF----LDASTGWSTWSN-PEA-----WGTTPSTGTI 320
 Db 267 GTYVFVQRCNPPIGYGSKRAGIWSENSHPTAASTPRSERPSPGGGACEPRGEPPSGCPV 326

QY 321 PKEIP--AWGQLH 331
 Db 327 RRELKQFLGWLKHH 340

RESULT 12
 US-09-880-578-29
 Sequence 29, Application US/09880578
 Patent No. US20020045733A1
 GENERAL INFORMATION:
 APPLICANT: Loh, Si
 Presnell, Scott R.
 Jelberg, Anna C.
 Gilbert, Teresa

RESULT 13
US-09-037-657-44
Sequence 44, Application US/09037657A
Patent No. US200405741A1
GENERAL INFORMATION:
APPLICANT: Hilton, Douglas J.
APPLICANT: Nicola, Nicos A.
APPLICANT: Farley, Allison
APPLICANT: Wilson, Tracy
APPLICANT: Zhang, Jian-Guo
APPLICANT: Alexander, Warren
APPLICANT: Rakar, Steven
APPLICANT: Fabri, Louis
APPLICANT: Kojima, Tetsuo
APPLICANT: Maeda, Masatsugu
APPLICANT: Kikuchi, Yasufumi
APPLICANT: Nash, Andrew
TITLE OF INVENTION: ENCODING SAME
TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR AND GENETIC SEQUENCES
FILE REFERENCE: DAVIES COLITON CAVE (CIP)
CURRENT APPLICATION NUMBER: US/09/037,657A
CURRENT FILING DATE: 1998-03-10
EARLIER APPLICATION NUMBER: 08/928,720
EARLIER FILING DATE: 1997-09-11
NUMBER OF SEQ ID NOS: 54
SEQ ID NO: 44
LENGTH: 421
TYPE: PRT
ORGANISM: Unknown
FEATURE:
OTHER INFORMATION: Description of Unknown Organism: Amino Acid Sequence of NR6
US-09-037-657-44

Query Match 9.38; Score 211.5; DB 10; Length 421;
Best Local Similarity 23.78; Pred. No. 3.9e-07;
Matches 91; Conservative 53; Mismatches 145; Indels 95; Gaps 19;

Qy 7 GLSRVLYVAVATALVASSPQAWGPPGVQYGPGRSVKLCC----PGVYTAGDPVSWF 60
Db 29 GAPRAGSGATTAVisQDPTLLI-----SSLATCVHGDPPATA-EGLYNW 76
Qy 61 RDGE--PKLIQGPDSLGHHLVLQAQD----SDDEGTYTCQTLDLGALGGTVTLQLGYP 112
Db 77 LNGRRLPPESRVLNAs--TLALALANLNGSQRSGDNLVCHARDGTSIAGSCLIVGLP 133
Qy 113 PARPV-VSCQADYENFSCTWSPSQ--ISGLPTRYLTSYKTVLGAQSRRSPTGPWP 169
Db 134 PEKPNVNSCKNMKDLCRWTGAHGETFLHTNVSLSKYLRWYCQDNTEBEYHVGPHS 193
Qy 170 C--PQDPLGAAARCVYHGAEFNSQYRINVTEVNPLG-ASTRLDLSQSLIRPDPPQGLRV 226
Db 194 CHIPD-----LAFTPYEWEATNRIGLSARSVDLTDIDVTTDPPDVH 242
Qy 227 ESYPGYPRRRASWTHPASWCPQPHFL--KERLQYRPBHPAWSVEP-----AG 275
Db 243 SRVGGLEDQLSYRWSP---PALKDFLFOQKYQIRYRVEDSVWVYDDYSNOTSCLRAG 299
Qy 276 LEEVITDAVGLPHAYRVSARDF----LDAGTWTWS-PEA----- 311
Db 300 LK-----POTVYFQVRNPFPFGYIGSKKAGIWISeWSHITAASPRSERPGPGGACEP 352
Qy 312 -WGTGSTGTIPKEIP---ANGQLH 331
Db 353 RGEPSSGPVRELKOFGLWLKKH 376

RESULT 14
US-09-944-413-32
Sequence 32, Application US/09944413
Patent No. US2002156004A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin
APPLICANT: Botstein, David
APPLICANT: Eaton, Dan
APPLICANT: Ferrara, Napoleone
APPLICANT: Filvaroff, Ellen
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul
APPLICANT: Grimaldi, Christopher
APPLICANT: Gurney, Austin
APPLICANT: Hillan, Kenneth
APPLICANT: Kjavin, Ivar
APPLICANT: Napier, Mary
APPLICANT: Roy, Margaret
APPLICANT: Tumas, Daniel
APPLICANT: Wood, William
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC ACIDS ENCODING THE SAME
FILE REFERENCE: P2548P1C1
CURRENT APPLICATION NUMBER: US/09/944,413
CURRENT FILING DATE: 2001-09-26
PRIOR APPLICATION NUMBER: 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/067,411
PRIOR FILING DATE: December 3, 1997
PRIOR APPLICATION NUMBER: 60/069,334
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,335
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,278
PRIOR FILING DATE: December 11, 1997
PRIOR APPLICATION NUMBER: 60/069,425
PRIOR FILING DATE: December 12, 1997
PRIOR APPLICATION NUMBER: 60/069,696
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,694
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,702
PRIOR FILING DATE: December 16, 1997
PRIOR APPLICATION NUMBER: 60/069,870
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/069,873
PRIOR FILING DATE: December 17, 1997
PRIOR APPLICATION NUMBER: 60/068,017
PRIOR FILING DATE: December 18, 1997
PRIOR APPLICATION NUMBER: 60/070,440
PRIOR FILING DATE: January 5, 1998
PRIOR APPLICATION NUMBER: 60/074,086
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/074,092
PRIOR FILING DATE: February 9, 1998
PRIOR APPLICATION NUMBER: 60/075,945
PRIOR FILING DATE: February 25, 1998
PRIOR APPLICATION NUMBER: 60/112,850
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 60/113,296
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: PCT/US98/19330
PRIOR FILING DATE: September 16, 1998
PRIOR APPLICATION NUMBER: PCT/US98/251,08
PRIOR FILING DATE: December 1, 1998
PRIOR APPLICATION NUMBER: 09/216,021
PRIOR FILING DATE: December 16, 1998
PRIOR APPLICATION NUMBER: 09/218,517
PRIOR FILING DATE: December 22, 1998
PRIOR APPLICATION NUMBER: 09/254,311
PRIOR FILING DATE: March 3, 1999
PRIOR APPLICATION NUMBER: PCT/US99/12252
PRIOR FILING DATE: June 22, 1999
PRIOR APPLICATION NUMBER: PCT/US99/21090

PRIOR FILING DATE: September 15, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28409
; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28313
; PRIOR FILING DATE: No. US20020156004A1ember 30, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/28301
; PRIOR FILING DATE: December 1, 1999
; PRIOR APPLICATION NUMBER: PCT/US99/30095
; PRIOR FILING DATE: December 16, 1999
; PRIOR APPLICATION NUMBER: PCT/US00/03565
; PRIOR FILING DATE: February 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/04414
; PRIOR FILING DATE: February 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/05841
; PRIOR FILING DATE: March 2, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/08439
; PRIOR FILING DATE: March 30, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/14042
; PRIOR FILING DATE: May 22, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: July 28, 2000
; PRIOR APPLICATION NUMBER: PCT/US00/32678
; PRIOR FILING DATE: December 1, 2000
; PRIOR APPLICATION NUMBER: PCT/US01/06520
; PRIOR FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO: 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
; US-09-944-413-32

Query Match 9.3% Score 211.5; DB 9; Length 422;
Best Local Similarity 23.7%; Pred. No. 3 9e-07;
Matches 91; Conserved 53; Mismatches 145; Indels 95; Gaps 19;

QY	7	GLSRVLYAVATLVASSSPCPAQAWGPPGVQYQPGRSVYKLCC-----PGVNTAGDPVSWF	60
Db	30	GAPRAGSGAHTAVISPQDPTL-----GSSLLATCSEVHGDPGATA-EGLIWT	77
QY	61	R DGE--PKLQGPDSGLGHELVLAQAD---STDEGTICOTLDGALGGTtVLQGYP	112
Db	78	LNGRRLPPLPSRVLNAs--TLALALANLNGQRSGDNLYCHARDGSILASSCLYVGLP	134
QY	113	PARY-VSQADYENFSCTWSPSQ--ISGLPPRYLTSYRKIVLGADSQRSPSTGWPW	169
Db	135	PEKVNISCWSKNMKDLCRWTGAAHGETFLTNNSLYKLYMQDNTCEYHTVGPHS	194
QY	170	CQDPLGAARCVBHGAEFWSSOYRINTNEVNPGLDVSLSILRDPPQQLRV	226
Db	195	CHIPKD-----LALFTPEIWTEATNRGSAASDVLTDILDQVTDPPPVDHV	243
QY	227	ESVPGYPRRLRASWTPASWPCOPHELL-KFRLQYRPAHQPAWSTVEP-----AG	275
Db	244	SRVGGLEDLSRVNVP--PALKDFELQAKYQIYRVEDSDWKVYDDVSNOTSCRLAG	300
QY	276	LEEVITDAVGLPHAVRSARDF----LDATGWSTWS-PEA-----	311
Db	301	LK-----PGTYFVQVRNCNPQGIYGSKKAQGWESENHSPTAASTPRSERPQPGGGACEP	353
QY	312	-WGTPSTGTIPKEP---AWGQLH	331
Db	354	RGGPSSGPVRELKQFLQWLKK	377

RESULT 15
; Sequence 32, Application US/09944403
; Patent No. US2002015143A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin
; APPLICANT: Botstein, David
; APPLICANT: Eaton, Dan

```

; PRIORITY FILING DATE: NO. US20020165143Aember 30, 1999
; PRIORITY APPLICATION NUMBER: PCT/US99/28301
; PRIORITY FILING DATE: December 1, 1999
; PRIORITY APPLICATION NUMBER: PCT/US99/30095
; PRIORITY FILING DATE: December 16, 1999
; PRIORITY APPLICATION NUMBER: PCT/US00/03565
; PRIORITY FILING DATE: February 11, 2000
; PRIORITY APPLICATION NUMBER: PCT/US00/04414
; PRIORITY FILING DATE: February 22, 2000
; PRIORITY APPLICATION NUMBER: PCT/US00/03841
; PRIORITY FILING DATE: March 2, 2000
; PRIORITY APPLICATION NUMBER: PCT/US00/08439
; PRIORITY FILING DATE: March 30, 2000
; PRIORITY APPLICATION NUMBER: PCT/US00/14042
; PRIORITY FILING DATE: May 22, 2000
; PRIORITY APPLICATION NUMBER: PCT/US00/20710
; PRIORITY FILING DATE: July 28, 2000
; PRIORITY APPLICATION NUMBER: PCT/US00/32678
; PRIORITY FILING DATE: December 1, 2000
; PRIORITY APPLICATION NUMBER: PCT/US01/05520
; PRIORITY FILING DATE: February 28, 2001
; NUMBER OF SEQ ID NOS: 120
; SEQ ID NO: 32
; LENGTH: 422
; TYPE: PRT
; ORGANISM: Homo Sapien
US-09-944-403-32

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Query Match          9.38;  Score 211.5;  DB 9;  Length 422;
Best Local Similarity 23.7%;  Pred. No. 3.9e-07;
Matches 91;  Conservative 53;  Mismatches 145;  Indels 95;  Gaps 19;
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Db   30 GAPRAGSGHTAVISQDPDTLLI-----GSSLATCSCVHGDPDATA-BGLYWT 77
Qy   61 RDGE--PKLQGPDSGLGHIELVLAQD-----STDEGTYCQTLDGAEGTVTQLGYP 112
Db   78 LNRRRLPPLSERVLNAS--TLALALANLNSQRSGDNVYCHARDGSITLAGSCLYYGLP 134
Qy   113 PARPV-VSCQADYENFSCTWPSQ - ISGLPTRYLTSSYKKTVLGADSRSRSPSTGPWP 169
Db  135 PEKPWNISCSNEKNMKDLTCKWTPGAHGETHTNYSLSKYLRWYGDNTCEEYHTVGPHS 194
Qy   170 C--PQDPLGAARCTVYHGAEFWSQRYINTEVNPLG - ASTRLDVSLOSSLRDPFGQLRV 226
Db  195 CHIPKD-----LAFTPYEWATEANLGSARSVDLTDLDVVTTDPPDVHV 243
Qy   227 ESVPGYPRRLRASWTPYASNPQCPHFL - KFRLQYRPQHPAWSTVEP-----AG 275
Db  244 SRVGGLEDQLSVRWVSP--PAKDLFLQARYQIRVVEDSDNRKVDDVSNOTSCRLAG 300
Qy   276 LEEVITDAVAGLPHAVRVSARDF---LDA GTWSTWS -DEA----- 311
Db  301 LK-----PCTVYFVQVRNPFGIYGSKAGIWI SEW SHTAASPRSERPGPGGGACEP 353
Qy   312 -WGTPTSTGTIPKEIP--AWCQLH 331
Db  354 RGEPSSGPVRELKOFGLNLKKH 377

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 Job time : 17 secs

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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: January 17, 2003, 19:36:45 ; Search time 18 Seconds
(without alignments)
689.804 Million cell updates/sec

Title: US-09-924-338-2

Perfect score: 2275

Sequence: 1 MSSSSGGLSRVLYAVATALV.....KPGFLASVIPVDRRGAPNL 422

Scoring table: BLOSUM62
Gapext 0.5

Searched: 262574 seqs, 29422922 residues

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:
5: /cgn2_6/ptodata/1/iaa/BCTUS.COMB.pep:
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:
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*
*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the total score distribution, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	2275	100.0	422	4	US-09-151-102-2	Sequence 2, Appli
2	2275	100.0	422	4	US-08-929-846-2	Sequence 2, Appli
3	2257.5	99.2	423	4	US-08-702-665A-5	Sequence 5, Appli
4	1897	83.4	432	4	US-08-702-665A-3	Sequence 3, Appli
5	1831	80.5	441	4	US-09-151-102-4	Sequence 4, Appli
6	1831	80.5	441	4	US-08-929-846-4	Sequence 4, Appli
7	382	16.8	372	4	US-09-211-590-2	Sequence 1, Appli
8	379	16.7	372	1	US-07-865-878A-4	Sequence 4, Appli
9	379	16.7	372	1	US-07-676-647-2	Sequence 2, Appli
10	379	16.7	372	1	US-08-449-329-2	Sequence 5, Appli
11	379	16.7	372	2	US-08-445-073-2	Sequence 2, Appli
12	379	16.7	372	2	US-08-585-258-2	Sequence 2, Appli
13	379	16.7	372	2	US-08-603-010-2	Sequence 2, Appli
14	379	16.7	372	5	PCT-US91-03896-4	Sequence 5, Appli
15	360	15.8	468	4	US-08-795-473B-5	Sequence 5, Appli
16	360	15.8	468	4	US-09-39-856-5	Patent No. 5171840
17	360	15.8	468	6	5171840-2	Patent No. 5171840
18	360	15.8	468	6	5480796-2	Patent No. 5171840
19	330	14.5	344	6	5171840-7	Patent No. 5171840
20	330	14.5	344	6	5480796-7	Patent No. 5171840
21	325	14.3	323	6	5171840-6	Patent No. 5171840
22	325	14.3	323	6	5480796-6	Patent No. 5171840
23	259.5	11.4	229	3	US-08-684-687-2	Sequence 2, Appli
24	259.5	11.4	229	3	US-08-352-678-6	Sequence 6, Appli
25	255.5	11.2	229	1	US-08-383-750-6	Sequence 6, Appli
26	240	10.5	230	5	PCT-US93-09636-6	Sequence 6, Appli
27	232	10.2	386	6	5171840-5	Patent No. 5171840

ALIGNMENTS

RESULT 1
US-09-151-102-2
; Sequence 2, Application US/09151102
; Patent No. 627447
; GENERAL INFORMATION:
; APPLICANT: Tobin, James
; TITLE OF INVENTION: HUMAN INTERLEUKIN-11 RECEPTOR
; NUMBER OF SEQUENCES: 4
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genetics Institute, Inc.
; STREET: 87 CambridgePark Drive
; CITY: Cambridge
; STATE: MA
; COUNTRY: USA
; ZIP: 02140
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/151.102
; FILING DATE:
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: 08/663,584
; FILING DATE: 14-JUN-1996
; APPLICATION NUMBER: 08/362,304
; FILING DATE: 22-DEC-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Brown, Scott A.
; REGISTRATION NUMBER: 32,724
; REFERENCE/DOCKET NUMBER: GI5252
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (617) 498-8224
; TELEFAX: (617) 876-5951
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 422 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-151-102-2

Query Match Score 100.0%; Best Local Similarity 100.0%; Pred. No. 1.e-173;
Matches 422; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MSSSGGLSRVLYAVATALVASSPCPQAWGGPPGVQYGPGRSVKLCCPGVTAGDPYSWF 60

US-08-929-846-2

Query Match 100.0%; Score 2275; DB 4; Length 422;

Best Local Similarity 100.0%; Pred. No. 1-4-e-173; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSSSGSLSRVLYAVATALYSASSPCPQAMGGPQGRSVKLCCPGVTAGDPVSMF 60

Db 61 RDGEPKLLOGPDSGLGHELVLAQADSTDEGTYICOTLDGAIGGTVTLQIGYPARPVSC 120

Qy 61 RDGEPKLLOGPDSGLGHELVLAQADSTDEGTYICOTLDGAIGGTVTLQIGYPARPVSC 120

Db 121 QAADENFSCTWSQISGLPTRYLTSYRKTKVLGADSRSRSPSTGPWPCPQDPLGAARC 180

Qy 121 QAADENFSCTWSQISGLPTRYLTSYRKTKVLGADSRSRSPSTGPWPCPQDPLGAARC 180

Qy 181 VVHGAEEFWSCYRINTVEPLGASTRLLDVSQSLTRPDPQGLRVESYPGYPRRLRASW 240

Db 181 VVHGAEEFWSCYRINTVEPLGASTRLLDVSQSLTRPDPQGLRVESYPGYPRRLRASW 240

Qy 241 TYPASWPCQPHFLKFRQLQYPAQHPMASTVEPAGLEEVITDAVGLPHAVRVSARDFLD 300

Db 241 TYPASWPCQPHFLKFRQLQYPAQHPMASTVEPAGLEEVITDAVGLPHAVRVSARDFLD 300

Qy 301 AGTGSTWSPEAWGTPSTGTIPKEPAWGLQHTOPEVEPQVDSAPPAPRSPSLOPHPRLDHR 360

Db 301 AGTGSTWSPEAWGTPSTGTIPKEPAWGLQHTOPEVEPQVDSAPPAPRSPSLOPHPRLDHR 360

Qy 361 DSVEQAVIALSIGLISFLGLVAGALAGLWLRLRGGRDGSPKGFLASVIVYDRRGAP 420

Db 361 DSVEQAVIALSIGLISFLGLVAGALAGLWLRLRGGRDGSPKGFLASVIVYDRRGAP 420

Qy 421 NL 422

Db 421 NL 422

RESULT 2

US-08-929-846-2

; Sequence 2, Application US/08929846

; Patent No. 6350855

; GENERAL INFORMATION:

; APPLICANT: Tobin, James

; TITLE OF INVENTION: HUMAN INTERLUKEKIN-11 RECEPTOR

; NUMBER OF SEQUENCES: 4

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Genetics Institute, Inc.

; STREET: 87 CambridgePark Drive

; CITY: Cambridge

; STATE: MA

; COUNTRY: USA

; ZIP: 02140

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/929, 846

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/663, 584

FILING DATE: 14-JUN-1996

FILING DATE: 22-DEC-1994

ATTORNEY/AGENT INFORMATION:

NAME: Brown, Scott A.

REGISTRATION NUMBER: 32,724

REFERENCE/DOCKET NUMBER: G15252

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 498-8224

TELEFAX: (617) 876-5851

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 422 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

SEQUENCE CHARACTERISTICS:

US-08-929-846-2

Query Match 100.0%; Score 2275; DB 4; Length 422;

Best Local Similarity 100.0%; Pred. No. 1-4-e-173; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSSSGSLSRVLYAVATALYSASSPCPQAMGGPQGRSVKLCCPGVTAGDPVSMF 60

Db 1 MSSSGSLSRVLYAVATALYSASSPCPQAWGPPGYQYGPGRSVYKLCPGVTAGDPVSMF 60

Qy 61 RDGEPKLLOGPDSGLGHELVLAQADSTDEGTYICOTLDGAIGGTVTLQIGYPARPVSC 120

Db 61 RDGEPKLLOGPDSGLGHELVLAQADSTDEGTYICOTLDGAIGGTVTLQIGYPARPVSC 120

Qy 121 QAADENFSCTWSQISGLPTRYLTSYRKTKVLGADSRSRSPSTGPWPCPQDPLGAARC 180

Db 121 QAADENFSCTWSQISGLPTRYLTSYRKTKVLGADSRSRSPSTGPWPCPQDPLGAARC 180

Qy 181 VVHGAEEFWSCYRINTVEPLGASTRLLDVSQSLTRPDPQGLRVESYPGYPRRLRASW 240

Db 181 VVHGAEEFWSCYRINTVEPLGASTRLLDVSQSLTRPDPQGLRVESYPGYPRRLRASW 240

Qy 241 TYPASWPCQPHFLKFRQLQYPAQHPMASTVEPAGLEEVITDAVGLPHAVRVSARDFLD 300

Db 241 TYPASWPCQPHFLKFRQLQYPAQHPMASTVEPAGLEEVITDAVGLPHAVRVSARDFLD 300

Qy 301 AGTGSTWSPEAWGTPSTGTIPKEPAWGLQHTOPEVEPQVDSAPPAPRSPSLOPHPRLDHR 360

Db 301 AGTGSTWSPEAWGTPSTGTIPKEPAWGLQHTOPEVEPQVDSAPPAPRSPSLOPHPRLDHR 360

Qy 361 DSVEQAVIALSIGLISFLGLVAGALAGLWLRLRGGRDGSPKGFLASVIVYDRRGAP 420

Db 361 DSVEQAVIALSIGLISFLGLVAGALAGLWLRLRGGRDGSPKGFLASVIVYDRRGAP 420

Qy 421 NL 422

Db 421 NL 422

RESULT 3

US-08-929-846-5

; Sequence 5, Application US/08702665A

; Patent No. 6274708

; GENERAL INFORMATION:

; APPLICANT: Hilton, Douglas J.

; TITLE OF INVENTION: A NOVEL HAEMOPOIETIN RECEPTOR

; NUMBER OF SEQUENCES: 25

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent In Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/702, 665A

FILING DATE: 20-DEC-1996

CLASSIFICATION: 536

ATTORNEY/AGENT INFORMATION:

NAME: Presser, Leopold

REGISTRATION NUMBER: 19,827

REFERENCE/DOCKET NUMBER: 10296

TELECOMMUNICATION INFORMATION:

TELEPHONE: (516) 742-4343

TELEFAX: (516) 742-4366

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:

LENGTH: 423 amino acids
 ;
 TYPE: amino acid
 ;
 TOPOLOGY: linear
 ;
 MOLECULE TYPE: protein
 US-08-702-665A-5

Query Match 99.2% Score 2257.5; DB 4; Length 423;
 Best Local Similarity 99.5%; Pred. No. 3.5e-172;
 Matches 421; Conservative 0; Mismatches 1; Gaps 1;

Query	Match	Score	Length
1 MSSCCSGLSRVIVAVATALYASSSPCQAWCPGVOYQOPGRSVKLCCPGYTAGDPVSWF 60	83.4%	1897	DB 4; Length 432;
Db 1 MSSCCSGLSRVIVAVATALYSSSPCQAWCPGVOYQOPGRSVKLCCPGYTAGDPVSWF 60	83.5%	1914	DB 4; Length 432; Pred. No. 1.9e-143; Mismatches 50; Indels 2; Gaps 1
Qy 61 RDGEPKLUQGPDSLGHVELVLAQADSTDEGYTICOTLDALGTYVLQLGYPPARPVSC 120	83.5%	1914	Best Local Similarity 83.5%; Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1
Db 61 RDGEPKLUQGPDSLGHVELVLAQADSTDEGYTICOTLDALGTYVLQLGYPPARPVSC 120	83.5%	1914	SEQUENCE CHARACTERISTICS: LENGTH: 432 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-702-665A-3
Qy 121 QADYENFSCWSQTSWPSQSLPRLPRYLISYRKTVLGAQDSQRSPSTGPWPQCDPLGAARC 180	83.5%	1914	Query Match 83.5%; Score 1897; DB 4; Length 432;
Db 121 QADYENFSCWSQTSWPSQSLPRLPRYLISYRKTVLGAQADSTDEGYTICOTLDALGTYVLQLGYPPARPVSC 180	83.5%	1914	Best Local Similarity 83.5%; Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1
Qy 181 VVHGAEEFWQSQTIRNTEVNPL-GASTRLLDVSLSQTLRDPDQGURVESVPGYPRRLRAS 239	83.5%	1914	SEQUENCE CHARACTERISTICS: LENGTH: 432 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-702-665A-3
Db 181 VVHGAEEFWQSQTIRNTEVNPLGASTRLLDVSLSQTLRDPDQGURVESVPGYPRRLRAS 240	83.5%	1914	Query Match 83.5%; Score 1897; DB 4; Length 432;
Qy 240 WTYPASWPCQPHFLKFRQLQYPAQHPAWSTVPEASLLEEVITDAVAGLPHAVRVSARDFL 299	83.5%	1914	Best Local Similarity 83.5%; Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1
Db 241 WTYPASWPCQPHFLKFRQLQYPAQHPAWSTVPEASLLEEVITDAVAGLPHAVRVSARDFL 300	83.5%	1914	SEQUENCE CHARACTERISTICS: LENGTH: 432 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-702-665A-3
Qy 300 DAGTWSWSPWAGTPSTGTIKEIIPAWGOLHTQPEVEPQVDSAPPRLDHS 359	83.5%	1914	Query Match 83.5%; Score 1897; DB 4; Length 432;
Db 301 DAGTWSWSPWAGTPSTGTIKEIIPAWGOLHTQPEVEPQVDSAPPRLDHS 360	83.5%	1914	Best Local Similarity 83.5%; Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1
Qy 360 RDSVEQAVLASIGLSFLGLVAGALGLWIRLRRGGKDGSPKPGFLASVTPVDRRPG 419	83.5%	1914	SEQUENCE CHARACTERISTICS: LENGTH: 432 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-702-665A-3
Db 361 RDSVEQAVLASIGLSFLGLVAGALGLWIRLRRGGKDGSPKPGFLASVTPVDRRPG 420	83.5%	1914	Query Match 83.5%; Score 1897; DB 4; Length 432;
Qy 420 PNL 422	83.5%	1914	Best Local Similarity 83.5%; Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1
Db 421 PNL 423	83.5%	1914	SEQUENCE CHARACTERISTICS: LENGTH: 432 amino acids TYPE: amino acid TOPOLOGY: linear MOLECULE TYPE: protein US-08-702-665A-3

RESULT 4
US-08-702-665A-3
Sequence 3, Application US/08702665A

GENERAL INFORMATION:
 APPLICANT: Hilton, Douglas J.
 TITLE OF INVENTION: A NOVEL HAEMOPOLETIN RECEPTOR
 NUMBER OF SEQUENCES: 25
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER
 STREET: 400 Garden City Plaza
 CITY: Garden City
 STATE: New York
 COUNTRY: United States of America
 ZIP: 11530

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DO/MS-DOS
 SOFTWARE: System Release #1.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/702,665A
 FILING DATE: 20-DEC-1996
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19 827
 REFERENCE/DOCKET NUMBER: 10296
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 APPLICATION NUMBER: 08/663,584

RESULT 5
US-09-151-102-4
Sequence 4, Application US/09151102
Patent No. 6274547
GENERAL INFORMATION:
 APPLICANT: Tobin, James
 TITLE OF INVENTION: HUMAN INTERLEUKIN-11 RECEPTOR
 NUMBER OF SEQUENCES: 4
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Genetics Institute, Inc.
 STREET: 87 CambridgePark Drive
 CITY: Cambridge
 STATE: MA
 COUNTRY: USA
 ZIP: 02140
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DO/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/151,102
 FILING DATE:
 CLASSIFICATION: 536
 ATTORNEY/AGENT INFORMATION:
 NAME: Presser, Leopold
 REGISTRATION NUMBER: 19 827
 REFERENCE/DOCKET NUMBER: 10296
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (516) 742-4343
 APPLICATION NUMBER: 08/663,584

```

FILING DATE: 14-JUN-1996
APPLICATION NUMBER: 08/362,304
FILING DATE: 22-DEC-1994
ATTORNEY/AGENT INFORMATION:
NAME: Brown, Scott A.
REGISTRATION NUMBER: 32,724
REFERENCE/DOCKET NUMBER: G15252
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 498-8224
TELEFAX: (617) 876-5851
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 441 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-151-102-4

Query Match Score 80.5%; Length 441;
Best Local Similarity 83.1%; Pred. No. 3.6e-138;
Matches 340; Conservative 17; Mismatches 50; Indels 2; Gaps 1;

Query 16 ATALVASSCPQIAGPPGYQQGEPGRSYKLCCPGVTAAGDPVSFRDGEPKLLOGPDGSL 75
Db 25 ATALVSSSSCPQIAGPPGYQQGEPGRSYKLCCPGVTAAGDPVSFRDGEPKLLOGPDGSL 75
Qy 76 GHELVLAQADSTDESYICCTLDGALGGTYWTLQGLGPAPVYSCQAQDWENFSCTWSPS 135
Db 85 GHRLVLAQDVSPDDESYCQLDGSGMVTKLGFPPARPEVSCQAQDWENFSCTWSPS 144
Qy 136 QISGLPTRYTTSYRKTKLQADSQRSPSTGPWPQPQDPIGAARCVHGAEFWSQYRINV 195
Db 145 QVSGLPTRYTTSYRKTKLQAESQDRESPSTGPWPICQDPDPLEASRCVHGAEFWSQYRINV 204
Qy 196 TEYNPLGASTRLLDVSQSLTRDPPQGLRVESYPGYPRRLRASWTYPAWSQPCPHFLK 255
Db 205 TEYNPLGASTCLLDRQSLTRDPPQGLRVESYPGYPRRLRASWTYPAWSRQPCPHFLK 264
Qy 256 FRQLYRPAHQHPANSTVEPAGLEEVITDAVGLPHAVRYSAQDFLDAGITWSPPAWGTP 315
Db 265 FRQLYRPAHQHPANSTVEPAGLEEVITDAVGLPHAVRYSAQDFLDAGITWSPPAWGTP 324
Qy 316 STGTIPKEPAWQOLHTQ - PEVYQVQDSPPAPRPSLOQPHPRLLDHRDSEVQAVLASIG 373
Db 325 STGPLQDEPQDSQHGQOLEAVVAQEDSPPAPRPSLOQPHPRLLDHRDSEVQAVLASIG 384
Qy 374 ILSFLGLIVAGALAGLWMLRRLRGKDGSPKGFLASVTPYDRRGAPNL 422
Do 385 IFSCLGLAVGALAGLWMLRRLRGKDGSPKGFLASVTPYDRRGAPNL 433

RESULT 6
US-08-929-846-4
Sequence 4, Application US/08929846
Patent No. 6350855
GENERAL INFORMATION:
APPLICANT: Tobin, James
TITLE OF INVENTION: HUMAN INTERLUKEIN-11 RECEPTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genetics Institute, Inc.
STREET: 87 Cambridge Park Drive
CITY: Cambridge
STATE: MA
COUNTRY: USA
ZIP: 02140
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compat
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929-846-4
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FILING DATE: CLASSIFICATION: 435
 PRIORITY APPLICATION NUMBER: 08/663,584
 FILING DATE: 14-JUN-1996
 APPLICATION NUMBER: 08/362,304
 FILING DATE: 22-DEC-1994
 ATTORNEY/AGENT INFORMATION:
 NAME: Brown, Scott A.
 REGISTRATION NUMBER: 32,724
 REFERENCE/DOCKET NUMBER: G15252
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (617) 498-0224
 TELEFAX: (617) 876-5851
 SEQUENCE FOR SEQ ID NO: 4 :
 SEQUENCE CHARACTERISTICS:
 LENGTH: 441 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US -08-929-846-4

	Query Match	Score 80.5%	DB 4;	Length 441;
	Best Local Similarity	83.1%	Pred. No. 3.	6e-138;
	Matches 340;	Conservative 17;	Mismatches 50;	Indels 2;
				Gaps 1;
Qy	16 ATAVLASSSSPCPQAWGPPGVQYQGPGRSVYKLCPGTYAGDPVSWFRDGEPKLILQGPDSGL	75		
Db	25 ATAVLSSSSPCPQAWGPPGVQYQGPGRYMLCPCPGVSAGETPVSWFRGDSRLLQGPDSGL	84		
Qy	76 GHRLVLQAQADSTDEGTYCOTLDGALGGTIVTLQGYPPARPVVSQADYENFSCTWSPS	135		
Db	85 GHRLVLQAQDVDSPEDEGTYCQTLQDGSGGAVTQLKGFPAPREVSQCAVDYENFSCTWSPG	144		
Qy	136 QISGLPLTRYLTSLRKTKTVLGADSQRSRSPSTGWPWCPQDPLGASARCYVHGAETWW6QYRINV	195		
Db	145 QVSGLPLTRYLTSLRKTKTLPGAESQRESPTSGWPWCPQDPLGASARCYVHGAETWW6QYRINV	204		
Qy	196 TEYNPLGASTRLDVSLTRDPPQGLREVSPYGRRLRASNTYPAWNPCQPHFLK	255		
Db	205 TEYNPLGASTCLDVRQLSTLRDPPQGLREVSPYGRRLRASNTYPAWNPCQPHFLK	264		
Qy	256 FRQYRPAQHPAINTVEPAGLEVITDAVGLPHAVRSARDFLDAGTWSTWSPEAWGTP	315		
Db	265 FRQYRPAQHPAINTVEPAGLEVITDAVGLPHAVRSARDFLDAGTWSTWSPEAWGTP	324		
Qy	316 STGTIPREIPAWNQLHTQ -PEPEQVDSAPAPRESLQPHPRLBHDRTSYEQAVALSLG	373		
Db	325 STGQPLDEPDQSOGHGQLEAVQAQEDSPAPARESLQDPPLHDRTDPLEQAVAVLASLG	384		
Qy	374 ILSFLGLVAGALGLWLRRLRGDKGSPKGFLASVTPDRPGAPNL	422		
Db	385 IFSCLGLVAGALGLWLRRLRGDKGSPKGFLASVTPDRPGAPNL	433		

RESULT 7
 US-09-211-590-2
 Sequence 2, Application US/09211590
 Patent No. 6316206

GENERAL INFORMATION:
 APPLICANT: Davis, Samuel Squinto, Stephen P.
 APPLICANT: Furth, Mark E.
 APPLICANT: Yancopoulos, George D.
 TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 NUMBER OF SEQUENCES: 15
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Pennie & Edmonds
 STREET: 1155 Avenue of the Americas
 CITY: New York
 STATE: U.S.A.
 COUNTRY: U.S.A.
 ZTP: 10036

COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/211,590
; FILING DATE: 05-09-2003
; CLASSIFICATION:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 07/676,647
; FILING DATE: 28-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Mistock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-082
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698854/9741
; TELEX: 66141 PENNIE
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-211-590-2

Query Match 16.8%; Score 382; DB 4; Length 372;
Best Local Similarity 30.1%; Pred. No. 8.6e-23;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

QY 12 LYAVATALVASSPCPAQWGPPOVYQGPGRSYKLCPGVTAGDPYSWERDGEPEKLUQGP 71
Db 12 VLAIAAAVVAQRHSQPE- APHQVYERLGSVDTLPGTAWDAIVTRVNGTD-- LAP 66

QY 72 DSSLGHELYLAQADSTDEGYICQTLDG- ALGTYTQLGTPPARPVISQQAADY- ENFS 129
Db 67 DLLNGSOLVLHGLGELGHSGLYCFHRDSWHRLHVGLPREFPLSCRNTYPRGFY 126

QY 130 CTHPSQISGLP- RYLTYSRKRTKTVLQADSQRSPSTGWPWCPQDPLGAARCVVHGAEFW 188
Db 127 CSWH-----LPPPTVIPNTFTVNLHGSK-----IMWEKDPAKRNCHIRYMHF 172

QY 189 S-QYRINVTEYNPLGASTRLLDVSQSLRDPQGLRVEVPGYPRRLRASWTPASW 246
Db 173 STIKYKVISNALGNATATADEFITVKDPPENVARVPNSNRLETVTWQPSIW 232

QY 247 PCQPHFLIKFRLQYRPAQHANSTVEPA- GLEEVTIDAVAGLPHAVYRSARDFLDGTWS 305
Db 233 PDPESFLPKFRLQYRPLDQHQVHLSGDTAHTITDAYKEYIIQYAAKD- NEIGTWS 291

QY 306 TWSPEANGTPSTGTCIPEKIPANGQLHTQPEVQFDSPAPPRPSLQPHPRLLDHDRTSVEQ 365
Db 292 DNSVAAHATPTEE- PRILTEAQ- AAETTSSTSSHAPP----PTTKICD----- 336

QY 366 VAVLASLGILSFLGVALGWLRLRGGRGDSPKPGFLASV 410
Db 337 -----FGEL-----GSGGGFSAFLVSV 354

RESULT 8
US-07-885-878A-4
Sequence 4, Application US/07865878A
; Sequence No. 5332672
; GENERAL INFORMATION:
; APPLICANT: Yancopoulos, George D. et al.
; TITLE OF INVENTION: Cell Free Ciliary Neurotrophic
; TITLE OF INVENTION: Factor/Receptor Complex
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas

RESULT 9
US-07-885-878A-4
Sequence 2, Application US/07676647
; Sequence 2, Application US/07676647
; Patent No. 5426177
; GENERAL INFORMATION:
; APPLICANT: Davis, Samuel
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Furth, Mark E.

APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/676,647
; FILING DATE: 1991/03/28
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-048
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: AMINO ACID
; TOPOLOGY: Linear
; MOLECULE TYPE: protein
; US-07-676-647-2

Query Match 16.7% Score 379; DB 1; Length 372;
Best Local Similarity 30.1%; Pred. No. 1.5e-22;
Matches 122; Conservative 47; Mismatches 161; Indels 68; Gaps 15;

QY 1.2 IYAVATALVASSPCCPAWGPVOQGPGRVEKILCPCPGVTPAGDPYSWFRDCEPKLQQP 71

DB 12 VIAAAAAYVYARHHSPE- -AHPVQERLGSVTLPCTGTAWDDAA/TWRYNGTD--LAP 6

QY 72 DSGLGHELVLAQADSDTDEGTYCQTLDG-AUGGTVLQLGPVPPAREVVSQADY-ENFS 129

DB 67 DILNGSOLVHLGELEGHSGLYACFHRSWHLRHQVLLHVGLP/PREFVLSCRNTYPKGY 126

QY 130 CTWSPSQISGLET-RYLTSYRKTVLGAQDSRSPSTGWPWCPQDPLGAARCVVHGAEFW 188

DB 127 CSWH----LPTPTVTPNTFNVTLHGSK----IMCEKDPAKRNCHIYMHF 172

QY 189 S-QYRINTEVNPLQGASTRLDVLSQSLTRPDPQGLRVEVPYPRRLRASWTYPASW 246

DB 173 STIKKVVISVNAQHNAATIDEFTIYKPDPPENVYARPVPSNPRRLTEVTQTPSTW 232

QY 247 PCQPHFLKFLRFLQYRPAQHPAWSTVEPA-GLEEVITDAYGLPHAVRVSARDFLDAGTWS 305

DB 233 PDPESPFLKFLRFLYRPLDQWQHVELSDQTAHTDAYKEYLIQVAKD-NEIGTWS 291

QY 306 TWSPBAWGPSTGTIPKEPAWGOIHTQPVEPOYDSDAPPRTSLOPHPRLLDHRDSYEQ 365

DB 292 DWSYAAAHATPWTEE PRHLTTEAQ- -AAETTTSTSSLAPP----PITKICD----- 336

QY 366 VAVLASGLSILSFLGLVAGAIALGLWLRLRGKGDKSPKGFLASY 410

DB 337 -----PGEL-----GGGGPCAPFLYSV 354

; APPLICANT: Davis, Samuel
; APPLICANT: Squinto, Stephen P.
; APPLICANT: Furth, Mark E.
; APPLICANT: Yancopoulos, George D.
; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pennie & Edmonds
; STREET: 1155 Avenue of the Americas
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/449,329
; FILING DATE: 05/07/97
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/700,677
; FILING DATE: 15-MAY-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Misrock, S. Leslie
; REGISTRATION NUMBER: 18,872
; REFERENCE/DOCKET NUMBER: 6526-065
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212 790-9090
; TELEFAX: 212 8698864/9741
; TELEX: 66141 PENNIE
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 372 amino acids
; TYPE: amino acid
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
; US-08-449-329-2

Query Match 16.7% Score 379; DB 1; Length 372;
Best Local Similarity 30.1%; Pred. No. 1.5e-22;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

QY 12 IYAVATALVASSPCCPAWGPVOQGPGRVEKILCPCPGVTPAGDPYSWFRDCEPKLQQP 71
Db 12 VLA AAAAAYVYARHHSPE- -AHPVQERLGSVTLPCTGTAWDDAA/TWRYNGTD--LAP 66
Qy 72 DSGLGHELVLAQADSDTDEGTYCQTLDG-AUGGTVLQLGPVPPAREVVSQADY-ENFS 129
Db 67 DILNGSOLVHLGELEGHSGLYACFHRSWHLRHQVLLHVGLP/PREFVLSCRNTYPKGY 126
Qy 130 CTWSPSQISGLET-RYLTSYRKTVLGAQDSRSPSTGWPWCPQDPLGAARCVVHGAEFW 188
Db 127 CSWH----LPTPTVTPNTFNVTLHGSK----IMCEKDPAKRNCHIYMHF 172
Qy 189 S-QYRINTEVNPLQGASTRLDVLSQSLTRPDPQGLRVEVPYPRRLRASWTYPASW 246
Db 173 STIKKVVISVNAQHNAATIDEFTIYKPDPPENVYARPVPSNPRRLTEVTQTPSTW 232
Qy 247 PCQPHFLKFLRFLQYRPAQHPAWSTVEPA-GLEEVITDAYGLPHAVRVSARDFLDAGTWS 305
Db 233 PDPESPFLKFLRFLYRPLDQWQHVELSDQTAHTDAYKEYLIQVAKD-NEIGTWS 291
Qy 306 TWSPBAWGPSTGTIPKEPAWGOIHTQPVEPOYDSDAPPRTSLOPHPRLLDHRDSYEQ 365
Db 292 DWSYAAAHATPWTEE PRHLTTEAQ- -AAETTTSTSSLAPP----PITKICD----- 336
Qy 366 VAVLASGLSILSFLGLVAGAIALGLWLRLRGKGDKSPKGFLASY 410
Db 337 -----PGEL-----GGGGPCAPFLYSV 354

RESULT 10
US-08-449-329-2
; sequence 2, Application US/08449329
; Patent No. 5648334
; GENERAL INFORMATION:

RESULT 11 US-08-445-073-2

Sequence 2, Application US/08445073
Patent No. 5849897
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furth, Mark E.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/445,073
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/676,647
FILING DATE: 28-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18-872
REFERENCE/DOCKET NUMBER: 6526-048
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-649741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-445-073-2

Query Match 16.7%; Score 379; DB 2; Length 372;
Best Local Similarity 30.1%; Pred. No. 1.5e-22;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

QY 12 LVAVATALVASSPCKPCQAWGPPCPVQKGPGRSYKLCPCGVTAQDPVSFRDGEPKLQGP 71
Db 12 VLAAGAAAVVAQRHSPQE -APHVQYERGSVDTLPCTANWDAATWRVNGTD-- LAP 66

QY 72 DSGLGHELVLAQADSTDEGTYCQTLDG-ALGTVTQLGYPARPVSCQADY-ENFS 129
Db 67 DLINGSQLVHLGJELGHSGLYACFHRSWHLRQVLLHVGGLPREPVLSCRSMNTYKGFY 126

QY 130 CTWSPSQISGLPT -RYLTSYRKTKTVLGADSQRSSPSTCPWPFCQDPLGARCYVHGAFW 188
Db 127 CSWH---LPIPTYIPTTFNVTVLHSK-----INVCEKDPAKJNRCHIRYMHLF 172

QY 189 S -QYRINTVEVNLPLGASTRLLDVSLSILRPDPQGIRVESVPGYPRRLRASWTFASW 246
Db 173 STIKYKVTSVSNALGHNATADEFITVKPDPPENYARVPNSNRFRTWQTPSTW 232

QY 247 PCQPHFLKFRQLQYRPAOHANSTVEPA-GLEEVITDAVGLPHAVRVSARDELDAFTWS 305
Db 233 PDPESFPLKFELYRPLLDDOMHVELSDGTAHTITDAYAGKEYIIQVAKD -NEIGTWS 291

QY 306 TWSPEANGTPSTGTIPKIPANGQLHTQPEVERQVDSPAPPRLQPHPRRLDHRDSVEQ 365

Db 292 DWVAHAATPWTETEPRHLTTEAQ -AETTUTSTSSSLAPP----PTTKICD----- 336
QY 366 VAYLASLGJLUSFGLVAGALAGLWLRLARRGGKDGSPKPGFLASV 410
Db 337 -----PGEL-----GSGGCPACPFLSV 354

RESULT 12 US-08-585-258-2

Sequence 2, Application US/08505258
Patent No. 582003
GENERAL INFORMATION:
APPLICANT: Davis, Samuel
APPLICANT: Squinto, Stephen P.
APPLICANT: Furth, Mark E.
APPLICANT: Yancopoulos, George D.
TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
NUMBER OF SEQUENCES: 15
CORESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/585,258
FILING DATE: 11-JAN-1996
CLASSIFICATION: 530
PRIORITY DATA:
PRIORITY NUMBER: 6526-065
APPLICATION NUMBER: US/08/001,904
FILING DATE:
APPLICATION NUMBER: US/07/00,677
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mistock, S. Leslie
REGISTRATION NUMBER: 18-872
REFERENCE/DOCKET NUMBER: 6526-065
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 372 amino acids
TYPE: amino acid
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-585-258-2

Query Match 16.7%; Score 379; DB 2; Length 372;
Best Local Similarity 30.1%; Pred. No. 1.5e-22;
Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

QY 12 LYAVATALVASSPCKPCQAWGPPCPVQKGPGRSYKLCPCGVTAQDPVSFRDGEPKLQGP 71
Db 12 VLAAGAAAVVAQRHSPQE -APHVQYERGSVDTLPCTANWDAATWRVNGTD-- LAP 66

QY 72 DSGLGHELVLAQADSTDEGTYCQTLDG-ALGTVTQLGYPARPVSCQADY-ENFS 129
Db 67 DLINGSQLVHLGJELGHSGLYACFHRSWHLRQVLLHVGGLPREPVLSCRSMNTYKGFY 126

QY 130 CTWSPSQISGLPT -RYLTSYRKTKTVLGADSQRSSPSTCPWPFCQDPLGARCYVHGAFW 188
Db 127 CSWH---LPIPTYIPTTFNVTVLHSK-----INVCEKDPAKJNRCHIRYMHLF 172

QY 189 S -QYRINTVEVNLPLGASTRLLDVSLSILRPDPQGIRVESVPGYPRRLRASWTFASW 246
Db 173 STIKYKVTSVSNALGHNATADEFITVKPDPPENYARVPNSNRFRTWQTPSTW 232

QY 247 PCQPHFLKFRQLQYRPAOHANSTVEPA-GLEEVITDAVGLPHAVRVSARDELDAFTWS 305
Db 233 PDPESFPLKFELYRPLLDDOMHVELSDGTAHTITDAYAGKEYIIQVAKD -NEIGTWS 291

QY 306 TWSPEANGTPSTGTIPKIPANGQLHTQPEVERQVDSPAPPRLQPHPRRLDHRDSVEQ 365

Db 127 CSWH-----LPIPTYIPTTFNVTVLHSK-----IMVCEKDPAKJNRCHIRYMHLF 172

QY 189 S -QYRINTVEVNLPLGASTRLLDVSLSILRPDPQGIRVESVPGYPRRLRASWTFASW 246

Db 173 STIKYKYSISVNALGHNATAITDEEFTIVKDPDENVARPVPSNPRRLETVWQTPSTW 232
 Qy 247 PCOPHFLKFLRQLQRPAHQPAWSTVEPA -GLEEVITDAVAGLPHAYRVSAARDFLDAGTWS 305
 Db 233 PDPESFKPKFLRQLPFLDQHVLSDGTAHTIDAYAKEYTIIQVAAD-NEIGTWS 291
 Qy 306 TWSPEANGTPSTGTKEIPAWGQLHTQPEYEQVQDPSAPPRLSLOQPHPRLLDHDRSVEQ 365
 Db 292 DMSVAAHATPNTEE-PHLTEAQ -AAETTSTTSSSLAP-----PTTKICD----- 336
 Qy 366 VAVLASIGLISFLGLVAGALALGLWLRLRQKGDKGSPKPGFLASV 410
 Db 337 -----PGEL-----GSGGGPCCAPLVSV 354

RESULT 13
 US-08-603-010-4
 ; Sequence 4, Application US/08603010
 ; Patent No. 5955290
 ; GENERAL INFORMATION:
 ; APPLICANT: Yancopoulos, George D. et al.
 ; TITLE OF INVENTION: Cell Free Ciliary Neurotrophic Factor/Receptor Complex
 ; NUMBER OF SEQUENCES: 6
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/603,010
 ; FILING DATE:
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/118,968
 ; FILING DATE: 09-SEP-1993
 ; APPLICATION NUMBER: US 07/801,562
 ; FILING DATE: 02-DEC-1991
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 6326-082
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 790-9090
 ; TELEX: 66141 PENNIE 4 :
 ; INFORMATION FOR SEQ ID NO: 4 :
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 372 amino acids
 ; TYPE: amino acid
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; US-08-603-010-4

Query Match 16.7%; Score 379; DB 2; Length 372;
 Best Local Similarity 30.1%; Pred. No. 1.5e-22;
 Matches 122; Conservative 4; Mismatches 168; Indels 68; Gaps 15;

Qy 12 IYAVATALYSASSPCPQANGPPGYQGQCRSVKLCCPGVYTAGDPVSFRDGEPKLQGP 71
 Db 12 VIAAAAYVYVQHRSPOE -APHYQYERLGSVTLPCTANWDAATWRYNGTD--LAP 66
 Qy 72 DSGLGHELVIAQADSTDGEYTCQFLDG -ALGGTIVQYPPARPVWSCQAADY-ENFS 129
 Db 67 DLNGSQLVHLGLELGHSGLYIACFHRSWHLRHQVLLHVGLPPREVLSCRNTYPKGFY 126

Qy 130 CTWSPSSQISGLPT -RYLTSYRKKKTVLQADSQRSPSTGWPWCPQDPBLGAARCVVHAEFW 188
 Db 127 CSWH-----LPTPTYLPNTENVTYLHSK-----IMCEKDPALKRNCHIRYMHF 172
 Qy 189 -QYRINTEVNPLGASTRLDVSLQSILRPDPPGLRVESPVGPYPRRLRASWTPASW 246
 Db 173 STIKYKYSISVNALGHNATAITDEFETIVKDPDENVARPVPSNPRRLEVWQTPSTW 232
 Qy 247 PCQPHFLKFLRQLQYRPAQHPAWSTVEPA -GLEEVITDAVAGLPHAYRVSAARDFLDAGTWS 305
 Db 233 PDPESEFLKEFYRPLDQHVLSDGTAHTIDAYAKEYTIIQVAAD-NEIGTWS 291
 Qy 306 TWSPEANGTPSTGTKEIPAWGQLHTQPEYEQVQDPSAPPRLSLOQPHPRLLDHDRSVEQ 365
 Db 292 DWSVAAHATPNTEE-PHLTEAQ -AAETTSTTSSSLAP-----PTTKICD----- 336
 Qy 366 VAVLASIGLISFLGLVAGALALGLWLRLRQKGDKGSPKPGFLASV 410
 Db 337 -----PGEL-----GSGGGPCCAPLVSV 354

RESULT 14
 PCT-US91-03896-2
 ; Sequence 2, Application PC/TUS9103896
 ; GENERAL INFORMATION:
 ; APPLICANT: Davis, Samuel E.
 ; APPLICANT: Squinto, Stephen P.
 ; APPLICANT: Furth, Mark E.
 ; APPLICANT: Yancopoulos, George D.
 ; TITLE OF INVENTION: The Ciliary Neurotrophic Factor Receptor
 ; NUMBER OF SEQUENCES: 15
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: PCT/US91/03896
 ; FILING DATE: 1991/06/03
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Misrock, S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 6526-065-2228
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: 212 790-9090
 ; TELEX: 66141 PENNIE 4 :
 ; INFORMATION FOR SEQ ID NO: 2 :
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 372 amino acids
 ; TYPE: AMINO ACID
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: protein
 ; PCT-US91-03896-2

Query Match 16.7%; Score 379; DB 5; Length 372;
 Best Local Similarity 30.1%; Pred. No. 1.5e-22;
 Matches 122; Conservative 47; Mismatches 168; Indels 68; Gaps 15;

Qy 12 LVAVATALYSASSPCPQANGPPGYQGQCRSVKLCCPGVYTAGDPVSFRDGEPKLQGP 71
 Db 12 VIAAAAYVYVQHRSPOE -APHYQYERLGSVTLPCTANWDAATWRYNGTD--LAP 66
 Qy 72 DSGLGHELVIAQADSTDGEYTCQFLDG -ALGGTIVQYPPARPVWSCQAADY-ENFS 129
 Db 67 DLNGSQLVHLGLELGHSGLYIACFHRSWHLRHQVLLHVGLPPREVLSCRNTYPKGFY 126
 Qy 72 DSGLGHELVIAQADSTDGEYTCQFLDG -ALGGTIVQYPPARPVWSCQAADY-ENFS 129

RESULT 15
 ; Sequence 5 , Application US/08795473B
 ; Patent No. 6237858

GENERAL INFORMATION:
 / APPLICANT: Galun, Ethan
 / APPLICANT: Nahot, Orit
 / APPLICANT: Blum, Herbert E.
 / TITLE OF INVENTION: A Pharmaceutical Composition for Treating
 / NUMBER OF SEQUENCES: 10
 / CORRESPONDENCE ADDRESS:
 / ADDRESSEE: Davidson, Davidson and Kappel, LLC
 / STREET: 1140 Avenue of the Americas
 / CITY: New York
 / STATE: New York
 / COUNTRY: USA
 / ZIP: 10036

COMPUTER READABLE FORM:
 / MEDIUM TYPE: 3.5 inch disk
 / COMPUTER: IBM PC compatible
 / OPERATING SYSTEM: PC-DOS/MS-DOS
 / SOFTWARE: MS-DOS EDITOR
 / CURRENT APPLICATION DATA:
 / APPLICATION NUMBER: US/08795473B
 / FILING DATE: 11-FEB-1997
 / CLASSIFICATION:
 / ATTORNEY/AGENT INFORMATION:
 / NAME: Davidson, Clifford M.
 / REGISTRATION NUMBER: 32,728
 / REFERENCE/DOCKET NUMBER: 963-1007
 / TELECOMMUNICATION INFORMATION:
 / TELEPHONE: (212)-997-1028
 / TELEFAX: (212)-997-1037
 / INFORMATION FOR SEQ ID NO: 5:
 / SEQUENCE CHARACTERISTICS:
 / LENGTH: 468 amino acids
 / TYPE: amino acid
 / TOPOLOGY: unknown

US-08-795473B-5

Query Match 15.8%; Score 360; DB 4; Length 468;
 Best Local Similarity 28.4%; Pred. No. 6.6e-21;
 Matches 129; Conservative 57; Mismatches 196; Indels 72; Gaps 19;

Qy 1 MSSCCSLSRLVLYATAVYASSPQPQANPPGVOYQGRSRVLUCCPQGVTAGD--PVS 58
 Db 2 LAVGCALLAALIAAPSAAL--APRRCPAQEYARGVLTSLLSDSVTLTCPGVEPEDNATVH 59
 Qy 59 WERDGEPLKLGPD-----SGLGHELLVLAQADSTDEESTYICQTDLGALGGTVLQLG 110

Db 67 DLLNGSQLVLHGGLGLEHSGSLYACPHRSWHLRHQVLLHVGLPPREPVLSRSNTYPKGFY 126
 Qy 130 CTWSPSGSIQSLPT-RYLTSTRKTKTVLGADSQRSPSTGPWPQCDPDLGAARCVVHAEFW 188
 Db 127 CSWH----LPTPTVPIPNTPNTVHLGSK-----INVCEKDPAKRCIRYMHF 172
 Qy 189 S---QYRINATEVNPLNPGASTRLLDVLSQSILRPDPQGLRVESVPYPRRLRASWTPASW 246
 Db 173 STIKYKVSISSNALGHNATAITFDEFITVKPDPNNVARVPNSNPRIEVTWOTPSW 232
 Qy 247 PCQPHFLKFLQYRPAQHPAWSTVEPA-GLEEVITDAVAGLPHAVRSARDFDLAGTWS 305
 Db 233 PDPESPFLKFLYRPLDQWQHVELSDGTAHTIDAVAGKEYLIOVAAKD-NEIGTWS 291
 Qy 306 TWSPEAWGTSTGTKEIPAWGQLETPQEVEPQVDSPAPRPSLQPHPRLLDHRSVEQ 365
 Db 292 DWSVAAHATPWTEE-FRHLTEAQ--AAETTTSTSSLAPP-----PTTKICD----- 336
 Qy 366 VAVLASLGILSFLGLYAGAALGLMLRLRGKGDKDGPKGFLASVY 410
 Db 337 -----PGEI-----GSGGCPCAPLTVSV 354

Db 60 W-----VLRKPAAGSHPSRWSVOLHDSGNNSCYRA-GRPAGTVHLLVD 111
 Qy 111 YPPARPVVSC-QAADYENFSCTWSQPQISGLPTRYLTSYRKKTVLGADSQRSPSTGP - PW 168
 Db 112 VPPEEPOLSCERKSPLSNVYCCEWGPRTSPSLTT-----KAVLVRKQNSPAEDFQE 163
 Qy 169 PC---PQDPLGAARCVHGAEEFWSYRNLGS-TRLLVLSLOSSILRDPQPG 223
 Db 164 PCQYSQESOKFSCQLAVPEGDS-SYIVSNCVASSVGSKFSTKQTFOGGGLQDPDPAN 221
 Qy 224 LRVESTPGYPRRLRASWTPASWPCOPHFLKFRLQYRPAQHPAMSTVEPAGLEE-VIT 281
 Db 222 ITVTAVARNPRWLSSVTQDPHSWN-SSFYRDLFELRYAERSKTFTWMYKDLQHHCVIH 280
 Qy 282 DAVAGLPHAVRSARFLDAGTWSTSWSPPEAMGTPSNTGTTIKEIPAMGQLHTQPEVEPQVD 341
 Db 281 DAWSGLRHVVOLRAQEFQGQEWSEWSPEAMGTWPE-----RSPPAENEVS 328
 Qy 342 SPAPPRLPSLQPHPRLLDHRSVEQVAV----LASLGILSFLGLVAGAALG----- 388
 Db 329 TPMQALTNNKDDNII-FRDSANATSLPVQDSSSYLPFTL-VAGGSLAFTLCLATVL 386
 Qy 389 ---LW-LRLRRGGKGDKSPKPKFLASVYPVDRP 417
 Db 387 REKKTWKLRALEGKTSMHPPYSLGGLVPERPRP 420

Search completed: January 17, 2003, 19:39:29
 Job time : 21 secs

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Gapop 10.0 , Gapext 0.5							
Searched: 908470 seqs, 133250620 residues							
Total number of hits satisfying chosen parameters: 908470							
Minimum DB seq length: 0							
Maximum DB seq length: 2000000000							
Post-processing: Minimum Match 0%							
Maximum Match 100%							
Listing first 45 summaries							
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2:	/SIDS2/godata/geneseq/geneseqp-emb1/AA1981.DAT:*						
3:	/SIDS2/godata/geneseq/geneseqp-emb1/AA1982.DAT:*						
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21:	/SIDS2/godata/geneseq/geneseqp-emb1/AA2000.DAT:*						
22:	/SIDS2/godata/geneseq/geneseqp-emb1/AA2001.DAT:*						
23:	/SIDS2/godata/geneseq/geneseqp-emb1/AA2002.DAT:*						
Pred. No. is the number of results predicted by chance to have a higher score than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.							
SUMMARIES							
Result No.	Score	Query Match	Length	DB ID	Description	Location/Qualifiers	
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2	2275	100.0	422	22	AAB3654	112..365	
3	2275	100.0	422	22	AAU0725	/label= Type-1-cytokine_region	
4	2275	100.0	422	23	AAE14613	366..390	
5	2275.5	99.2	423	17	AAR92814	/label= Transmembrane_domain	
6	1897	83.4	432	17	AAR92813	391..422	
7	1871	82.2	432	22	AAB3653	/label= Intracellular_domain	
8	1831	80.5	441	17	AAR93091		
9	1831	80.5	441	22	AAU0726		
10	1831	80.5	441	23	AAE14614		

RESULT 3	
Qy	361 DSVEQAVAVLASIGLISFLGLVAGALGWLRLRGKGDKSPKPOFLASVIPVDRPGAP 4 20
Db	361 DSVEQAVAVLASIGLISFLGLVAGALGWLRLRGKGDKSPKPOFLASVIPVDRPGAP 4 20
Qy	421 NL 4 22
Db	421 NL 4 22
XX	AAU07725 standard; Protein: 422 AA.
XX	AAU07725;
AC	
XX	04-DEC-2001 (first entry)
XX	Human interleukin 11 receptor, IL-11R.
DE	
FH	Key
Peptide	peptide
FT	FT
FT	1..22
FT	label= "Signal_peptide"
FT	/note= "Alternative signal peptide"
Peptide	peptide
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Peptide	peptide
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FT	23..422
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Domain	domain
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FT	23..111
FT	label= "Immunoglobulin_like_domain"
Domain	domain
FT	FT
FT	24..365
FT	label= "Extracellular_domain"
FT	/note= "This sequence is specifically claimed in claim 1, this domain may start at residue 23."
Region	region
FT	FT
FT	24..359
FT	/note= "This sequence is specifically claimed in claim 1."
Region	region
FT	FT
FT	24..345
FT	/note= "This sequence is specifically claimed in claim 1."
Region	region
FT	FT
FT	24..324
FT	/note= "This sequence is specifically claimed in claim 1."
Protein	protein
FT	FT
FT	24..422
FT	label= "Mature_IL-11R"
FT	/note= "Alternative mature protein"
Protein	protein
FT	FT
FT	26..422
FT	label= "Mature_IL-11R"
FT	/note= "Alternative mature protein"
Region	region
FT	FT
FT	102..365
FT	/note= "This sequence is specifically claimed in claim 2."
Domain	domain
FT	FT
FT	112..365
FT	label= "Type_I_cytokine_domain"
Domain	domain
FT	FT
FT	366..390
FT	/label= "Transmembrane_domain"
Domain	domain
FT	FT
XX	US6274547-B1.

CC from adult mouse liver cDNA libraries. Nr1 is a low affinity
 CC receptor for IL-11 and interacts with gp130 to generate a high
 CC affinity IL-11 receptor. IL-11 can be used to develop
 CC agonists or antagonists of therapeutic apnl. or in the treatment
 CC or diagnosis of conditions involving a deficiency of IL-11,
 CC excess IL-11 or aberrant effects of normal endogenous IL-11
 XX

Sequence 432 AA;

Query Match 83.4%; Score 1897; DB 17; Length 432;
 Best Local Similarity 83.5%; Pred. No. 2.7e-124;
 Matches 354; Conservative 18; Mismatches 50; Indels 2; Gaps 1;

QY 1 MSSSCSGLRSRVAYATAVLYSASSPCPOANCPGQYQGQGRSVKLCCPGVYTAGDPVSWF 60
 Db 1 MSSSCSGLRTLVAYATAVLYSASSPCPOANCPGQYQGQGRSPVYLCCPGVYTAGDPVSWF 60
 QY 61 RDGEPKLQDGSGLGHELVIAQADSTDEGYICOTLDGAAGGTWTLQGYPPARPVSC 120
 Db 61 RDGDSRLQDGSGLGHRLVLAQDSDPDEGYVCTLDGVSGMWYILKGFPAPRVEVSC 120
 QY 121 QADDYENFSCTWSPSQISGLPTRYLTYSRKTKVTLGADSRSRSPSTGPWPCPQDPGLAARC 180
 Db 121 QADDYENFSCTWSPQVSGLPTRYLTYSRKTLPAESQRESPTGPWPCPQDPLEASRC 180
 QY 181 VVHGAEFWSOYRINTVEVNPFLGASTRLDVSQSLTRDPPQPLRVESTPGYPRRLRASW 240
 Db 181 VVHGAEFWSOYRINTVEVNPFLGASTRLDVSQSLTRDPPQGLRVESTPGYPRRLRASW 240
 QY 241 TYPASWPQCPHFLKFRQLYRPAQHPAWSTVEPAGLEENVTDAGVLPHAVRYSARDFLD 300
 Db 241 TYPASWRQCPHFLKFRQLYRPAQHPAWSTVEPAGLEENVTDAGVLPHAVRYSARDFLD 300
 QY 301 AGTWAFTWSPEAWGTPSTGTIPIKEPAWGLHTQ - PEVEPQVDSPAPPSPLOPHPRLLD 358
 Db 301 AGTWAFTWSPEAWGTPSTGTIPIKEPAWGLHTQDEPDWSOGHQOLEAVVAQEDSPAPPSPLODPRPID 360
 QY 359 HRDSYEQVAVLASIGLSLFIGLVAGALGLWLRLRGKGDKGSPKPGFLASVLPVDRPG 418
 Db 361 HRDPLEQVAVLASIGLSLFIGLVAGALGLWLRLRGKGDKGSPKPGFLASVLPVDRPG 420
 QY 419 APNL 422
 Db 421 IPNL 424

RESULT 7
 AAB36653 standard; protein: 432 AA.
 ID AAB36653
 AC AAB36653;
 XX 13-MAR-2001 (first entry)
 DE Mouse IL-11 receptor subunit alpha protein SEQ ID NO:10.
 KW DNAX cytokine receptor subunit; DCRS2; receptor protein;
 KW modulating cell proliferation; diagnosis; detection; drug screening;
 KW immunological disorder.
 OS Mus sp.
 PN WO200073451-A1.
 XX 07-DEC-2000.
 XX 30-MAY-2000; 2000WO-US14867.
 PR 01-JUN-1999; 99US-0322913.
 PA (SCHERING CORP.

PI Dowling LM, Timans JC, Gorman DM, Kastelein RA, Bazan FU;
 XX DR WPI; 2001-061536/07.
 XX PT Novel composition comprising DNAX cytokine receptor subunit protein function and for treating
 PT useful for regulating immune system function and for treating
 PT immunological disorders -
 XX Disclosure; Page 13-15; 93pp; English.
 XX
 CC The present invention describes a composition (I) comprising a recombinant DNAX cytokine receptor subunit-2 (DCRS2) polypeptide.
 CC The DCRS2 polypeptide is useful for binding ligands and for repairing cell
 CC antibodies. The DCRS2 polypeptide is also useful for modulating cell
 CC proliferation, for diagnostic and therapeutic applications, for
 CC detecting presence of their ligands and in drug screening assays. It
 CC is also useful for treating conditions such as immunological disorders.
 CC The present sequence represents a cytokine receptor subunit protein
 CC which is given in an alignment of various cytokine receptor subunits in
 CC the exemplification of the present invention.
 XX Sequence 432 AA;

Query Match 82.2%; Score 1871; DB 22; Length 432;
 Best Local Similarity 82.5%; Pred. No. 1.8e-122;
 Matches 350; Conservative 19; Mismatches 53; Indels 2; Gaps 1;
 QY 1 MSSSCSGLRSVYAYATAVLYSASSPCPOANCPGQYQGQGRSVKLCCPGVYTAGDPVSWF 60
 Db 1 MSSSCSGLRTLVAYATAVLYSASSPCPOANCPGQYQGQGRSPVYLCCPGVYTAGDPVSWF 60
 QY 61 RDGEPKLQDGSGLGHELVIAQADSTDEGYICOTLDGAAGGTWTLQGYPPARPVSC 120
 Db 61 RDGDSRLQDGSGLGHRLVLAQDSDPDEGYVCTLDGVSGMWYILKGFPAPRVEVSC 120
 QY 121 QADDYENFSCTWSPSQISGLPTRYLTYSRKTKVTLGADSRSRSPSTGPWPCPQDPGLAARC 180
 Db 121 QADDYENFSCTWSPQVSGLPTRYLTYSRKTLPAESQRESPTGPWPCPQDPLEASRC 180
 QY 181 VVHGAEFWSOYRINTVEVNPFLGASTRLDVSQSLTRDPPQPLRVESTPGYPRRLRASW 240
 Db 181 VVHGAEFWSOYRINTVEVNPFLGASTRLDVSQSLTRDPPQGLRVESTPGYPRRLRASW 240
 QY 241 TYPASWPQCPHFLKFRQLYRPAQHPAWSTVEPAGLEENVTDAGVLPHAVRYSARDFLD 300
 Db 241 TYPASWRQCPHFLKFRQLYRPAQHPAWSTVEPAGLEENVTDAGVLPHAVRYSARDFLD 300
 QY 301 AGTWAFTWSPEAWGTPSTGTIPIKEPAWGLHTQ - PEVEPQVDSPAPPSPLOPHPRLLD 358
 Db 301 AGTWAFTWSPEAWGTPSTGTIPIKEPAWGLHTQDEPDWSOGHQOLEAVVAQEDSPAPPSPLODPRPID 360
 QY 359 HRDSYEQVAVLASIGLSLFIGLVAGALGLWLRLRGKGDKGSPKPGFLASVLPVDRPG 418
 Db 361 HRDPLEQVAVLASIGLSLFIGLVAGALGLWLRLRGKGDKGSPKPGFLASVLPVDRPG 420
 QY 419 APNL 422
 Db 421 IPNL 424

RESULT 8
 AAR9091 standard; protein: 441 AA.
 ID AAR9091;
 XX AC AAR9091;
 XX DT 09-OCT-1996 (first entry)
 XX DE Murine Etl-2 gene product.
 KW Interleukin-11 receptor; IL-11 receptor; antibody; antagonist; bone;
 KW osteoporosis; Paget disease; myeloma; Etl-2.

(tartrate-resistant acid phosphatase) and bone marrow formation assays can be used for the identification of IL-11 antagonists. The method not only inhibits bone resorption and hence bone loss, but also increases the process of bone formation to increase bone density.

RESULT	12	Score	771;	DB	23;	Length	257;
BB006126		Best Local Similarity	33.9%;		Pred.	No. 4	8e-46;
		Matches	61.5%;		Mismatches	42;	Gaps
		Conservative	14;		Indels	44;	
ABB06126	ABB06126 standard; Protein; 257 AA.						
10-MAY-2002	(first entry)						
Human NS protein sequence SEQ ID NO:218.							
Human; cytosatic; osteopathic; gynaecological; neuroprotective; antirheumatic; antiarthritic; antipsoriatic; ophthalmological; anti-HIV; vasoconstrictor; antiarteriosclerotic; antiinflammatory; dermatological; aurorectic; muscular; antifertility; cardiovascular; anticoagulant; antifibrinolytic; hypotension; antiasthmatic; immunomodulator; cardiant; anticonvulsant; antidiabetic; tranquilliser; antidepressant; aeuoleptic; gastrointestinal; viricide; antilice; cerebroprotective; nootropic; contraceptive; vaccine; gene therapy; cancer; osteoporosis; dystonia; endometriosis; degenerative disease; multiple sclerosis; psoriasis; rheumatoid arthritis; cataract; restenosis; atherosclerosis; glaucoma; inflammation; skin disorder; obesity; muscular dystrophy; AIDS; infertility; cardiovascular disease; coagulation disease; hypertension; ischaemia; asthma; immune disease; epilepsy; angina; neurodegeneration; diabetes; anxiety; depression; schizophrenia; viral disease; stroke; gastric ulcer; Alzheimer's disease.							
Homo sapiens.							
W0200206315-A2.							
24-JAN-2002.							
17-JUL-2001; 2001WO-IL00653.							
Query Match	51	VTAGDP-PVSWERDGEPAKLLQGPDGLGHETLIAQADSTDEGYICQTLDGALG-----GT	104				
Db	1	MASGVPLSLGVDGCCELVRSQSPRGVGH-----SAAGTIDEDQQLRRAEQGPGGRGTSQGV	56				
Qy	105	VTLQL-----GYPARPVYSCQADYENFSCTWSPSQI	137				
Db	57	CLLPPLPFGLPGRGPVWAQRVREAVYLWSDCRDPPARPVYSCQADYENFSCTWSPSQI	116				
Qy	138	SGLPTRLTTSRKTKTVLGADSRRSSTGPMPCPQDPLGAARCVVIGAEFNSQYRNIVTE	197				
Db	117	SGLPTRLTTSRKTKTVLGADSRRSSTGPMPCPQDPLGAARCVVIGAEFNSQYRNIVTE	176				
Qy	198	VNPILGASTRLDVLSQSLIRDPDPPQGLRVEVPGYPRRLRASWNTYDASWPCSPSSSV	236				
Db	177	VNPLGASTRLDVLSQSLIRDPDPPQGLRVEVPGYPRRLRASWNTYDASWPCSPSSSV	236				
Qy	253	LLKFRLQYRPAGHPANTVE	272				
Db	237	CSTVRRIQPG-PRNSQLD	254				
RESULT	13						
AAR22616							
ID	AAR22616	standard; Protein;	460 AA.				
XX							
AC	AAR22616;						
IL-6R	04-NOV-1992	(first entry)					
DE	XX						
	DE	IL-6R for soluble IL-6R prodn.					

Db	382	FILRLQKWRSEAEKESKTTSPQQPSLKPFLVPLLVPLTPSSGSDN	433
XX	Soluble; sIL-6R.		
XX	KW		
XX	OS		
Mus musculus.			
XX	Key	Location/Qualifiers	
FH	1..19		
FT	/label= sig_Peptide		
FT	358..385		
Region	/note= "see CC"		
XX	JP04099800-A.		
XX	PN		
XX	PD	31-MAR-1992.	
XX	FT	XX	
PF	17-AUG-1990;	90JP-0215986.	
XX	PR	17-AUG-1990;	90JP-0215986.
XX	PR	WPI: 1992-157367/19.	
DR	P-PSDB; ARR22656.		
XX	PT	Recombinant mouse IL-6 receptor - prep'd. by culturing host	
PT	transformed by expression vector contng. DNA coding the protein,		
PT	and collecting soluble prod.		
XX	PS	Fig 7(1-2); 9pp; Japanese.	
XX	CC	The sequence is the full-length mouse IL-6 receptor.	
CC	CC	The region comprising amino acids 358-385 (see feature table)	
CC	CC	is indicated but not labelled in the sequence given in the	
CC	CC	specification. The sequence is used in the prodn. of a sol.	
CC	CC	mouse IL-6 receptor protein ('sIL-6') which binds specifically to	
CC	CC	IL-6 and has no intracellular region.	
XX	SQ	Sequence 460 AA;	
Query Match	17 4%	Score 395.5; DB 13; Length 460;	
Best Local Similarity	30.7%	Pred. No. 1.4e-19;	
Matches	145; Conservative	Mismatches 178; Indels 91; Gaps 25;	
Db	115 LSCFKRNPKLNNAICEWRPSSTPS-PTTKAWFLAKKI----NTNGKSDPQVQYSQQL 168		
Qy	1 MSSSGSGLSRVLYAVATALYSSASSPCPQAMGPPGVQYGPGRSYKLCCPQVTAQDVS - 58		
Db	2 LTVGCTLLVALLAAPAVLWGS --CRALEYANSTVTSLFGATVYLICKEAGNVTH 59		
Qy	59 WFRDGPKLJLQGPD-SGLGHELVLQAQDSTDGEETYICQTLDALGCTVTLQLGYPPARPV 117		
Db	60 WYSSS---QNREWTTGTITLVLRDVQLSDTGDYLCL-STNDHLVGTVPVLVDVPEEPK 114		
Qy	118 VSC-QAADYEFNESTWSPSQISGLPTRYLTYSRKTVLGADSQRSPSTQWPWPCP-QDPL 175		
Db	119 KSFSCQVEILEGGDKVHYHISLCVANSVGSKSSHNEAFHSIK-MYQDPDPANLVSAIPGR 227		
Qy	233 PRRRLRASWTYPAWNPCQPHFLKFRLQYRAQHPAWS ----TVEPAGIEEVITDAYG 286		
Db	228 PRWLKVSWQPEWTND-PSYLYLQFQLRYR ---PVWSKERTVLLPVAOQCVHDALRG 282		
Qy	287 LPHAVRVSAFDLQGATWTSWPSAAGTGTSTGTTPKEIKA --WGLQHTQPEVFBQVDS 343		
Db	283 VKHVWQVRKGKELQGOWNSPEVTGTPMIAE-PRTTAGILWNP--TQSVE--DS 335		
Qy	344 APPREPLSLQPHPRLDHRD----SVEQVAVIA-----SLEGSFLGQYQDQSSMSLPFL-VAGGSLAGLLC 390		
Db	336 -----ANHEDQYESSTEATSVLAPVOESSMSLPFL-VAGGSLAGLLC 381		
Qy	391 -----GSPKPGFLIASVTPVDRRPGAPN 421		
Db	169 KSFSCQVEILEGGDKVHYHISLCVANSVGSKSSHNEAFHSIK-MYQDPDPANLVSAIPGR 227		
Qy	176 GAARCVHGAEEFWSQYRI-NYTEVNFLGASTRLDW--SLOSTLRPDPQGLRVESVPGY 232		
Db	175 LSCFRKPNPLVNAICEWRPSSTPS-PTTKAVLFAKKI----NTNGKSDPQVQYSQQL 168		
Qy	176 GAARCVHGAEEFWSQYRI-NYTEVNFLGASTRLDW--SLOSTLRPDPQGLRVESVPGY 232		
Db	175 VSC-QADYEFNESTWSPSQISGLPTRYLTYSRKTVLGADSQRSPSTQWPWPCP-QDPL 175		
Qy	176 GAARCVHGAEEFWSQYRI-NYTEVNFLGASTRLDW--SLOSTLRPDPQGLRVESVPGY 232		
Db	175 LSCFRKPNPLVNAICEWRPSSTPS-PTTKAVLFAKKI----NTNGKSDPQVQYSQQL 168		
Qy	176 GAARCVHGAEEFWSQYRI-NYTEVNFLGASTRLDW--SLOSTLRPDPQGLRVESVPGY 232		
Db	175 VSC-QADYEFNESTWSPSQISGLPTRYLTYSRKTVLGADSQRSPSTQWPWPCP-QDPL 175		

Qy 233 PRLRASWTPASWPQPHFLKFLKERLQYRPAQHPAWS-----TVEPAGLEEVITDAVAG 286
 Db 228 PWLKYTSWQHPPFTWD-PSYVUILLQFLRYR----PWNSKEETVILLIPVAQYCQVIIHDALRG 282

Qy 287 LPHAVRVSARDFLDAGTWSTWSPEANGTPSTGTPKIPA--WGOILHTQPEVEPOVDSP 343
 Db 283 VKHVYQVRGKEEFLGOWSEENSPVETGTPWAE-PRTTPGILWNP-TQVSVE--DS- 335

Qy 344 APPRPSTLQPHPRLLDHRD---SVEQAVLA-----SLGILSFLGLVAGALALGLW--- 390
 Db 336 -----ANHEDQYSSESTEATSVLAPQESSSMSLPTFL-VAGGLAFLGLLCV 381

Qy 391 ---LRLRGKKD-----GSPKPGFLASVTPVDRRGAFN 421
 Db 382 FFLRLRQKWKSEAEKESKTTSPPPPYSLCPKPFLLPLTPHSSGSN 433

RESULT 15
 ID AAR13318 standard; Protein; 460 AA.
 XX
 AC AAR13318;
 XX
 DT 22-OCT-1991 (first entry)
 XX
 DE IL-6 receptor.
 XX
 KW Interleukin.
 XX
 OS Mus musculus.
 XX
 PN JP03155795-A.
 XX
 PD 03-JUL-1991.
 XX
 PF 13-NOV-1989; 89JJP-0292230.
 XX
 PR 13-NOV-1989; 89JJP-0292230.
 XX
 PA (KISHI/.) KISHIMOTO C.
 XX
 WPT; 1991-241723/33.
 DR N-PSDB; AAQ13113.
 XX
 PT Receptor protein of mouse IL-6 - prepd. by coding DNA sequence
 PT enabling mass-prod., and useful in study of IL-6 receptor or
 PT immune protein.
 XX
 PS Claim 1; Fig 2; 10pp; Japanese.

CC The amino acid sequence shown encodes mouse IL-6 receptor protein
 CC It can be used for study of the IL-6 receptor or immune mechanism
 CC The protein can be mass-produced by expression of the DNA in host
 CC cells.
 XX
 SQ Sequence 460 AA;

Qy 176 GAARCVVHGAEEFWSQYRI-NYTEVNPLGASTRLDV-SLOSTLRDPPOQLRVESSPGY 232
 Db 169 KSFSCQTEILLEDKVYHIVSCLCVANSVGSKSQNEAHSUK-MVQDPDPANUVVAAIGR 227

Qy 233 PRLRASWTPASWPQPHFLKFLKERLQYRPAQHPAWS-----TVEPAGLEEVITDAVAG 286
 Db 228 PWLKYSWQHPPFTWD-PSYVUILLPQFLRYR----PWNSKEETVILLIPVAQYCQVIIHDALRG 282

Qy 287 LPHAVRVSARDFLDAGTWSTWSPEANGTPSTGTPKIPA--WGOILHTQPEVEPOVDSP 343
 Db 283 VKHVYQVRGKEEFLGOWSEENSPVETGTPWAE-PRTTPGILWNP-TQVSVE--DS- 335

Qy 287 LPHAVRVSARDFLDAGTWSTWSPEANGTPSTGTPKIPA--WGOILHTQPEVEPOVDSP 343
 Db 283 VKHVYQVRGKEEFLGOWSEENSPVETGTPWAE-PRTTPGILWNP-TQVSVE--DS- 335

Qy 344 APPRPSIQPHPRLLDHRD---SVEQAVLA-----SIGLSFLGLVAGALALGLW--- 390
 Db 336 -----ANHEDQYSSESTEATSVLAPQESSSMSLPTFL-VAGGLAFLGLLCV 381

Qy 391 ---LRLRGKKD-----GSPKPGFLASVTPVDRRGAFN 421
 Qy 391 ---LRLRGKKD-----GSPKPGFLASVTPVDRRGAFN 421
 Db 382 FFLRLRQKWKSEAEKESKTTSPPPPYSLCPKPFLLPLTPHSSGSN 433

Search completed. January 17, 2003, 19:37:59
 Job time : 44 sees

Query Match	16.8%	Score	382.5;	DB	12;	Length	460;		
Best Local Similarity	30.3%	Pred.	No.	1.e-18;					
Matches	143;	Conservative	58;	Mismatches	180;	Indels	91;	Gaps	25;

Qy 1 MSSSCSGLISRVRLVAVATALVASSSPCQAWGGPPGYQGPGRSVKLUCPGTAGDPVS--
 Db 2 LTVGCCTLVALLAAPAVALVGS-CRALEYANGTTSLPLATVTLICPGREAAGNTIH 59

Qy 59 WFRDGEPKLQGPD-S-SGLGHIELVLAQADSTDEGYTCQTLGALGGTYTQLGYPPARPV 117
 Db 60 WVYSGS---QNREWTTGNTRVLDRYQLRGTGDLC-SLNDHLVGTVPPLVDVPPPEPK 114

Qy 118 VSC-QAADYENFSCTWPSQSLGLPRLYRLTSYRKRTVLGAASQRRRPSTGWPWPCP-QDPL 175
 Db 115 LSCFRKNPLVNAICENRPSSTS-PTTKAVLFAKKI---NTTNGKSDFQVPCQYSQQL 168

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